## November 2005

Published\_Applications Nucleic Acid and Published\_Applications Amino Acid database searches now generate two sets of results each. The Published\_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published\_Applications\_New databases; older published applications make up the Published\_Applications\_Main databases.

Searches run against Nucleic Acid Published\_Applications produce two sets of results, with the extensions .rnpbm (Published\_Applications\_NA\_Main) and .rnpbm (Published\_Applications\_NA\_New).

Searches run against Amino Acid Published\_Applications produce two sets of results, with the extensions .rapbm (Published\_Applications\_AA\_New).

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FEATURE:
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38827, A
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Sequence 60963, A
                                                                                                                                                                              March 7, 2006, 21:59:17; Search time 93.6 Seconds (without alignments) 107.136 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Published Applications AA_Main:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-10-751-235-4

US-10-751-235-1

US-10-751-235-18

US-10-751-235-18

US-10-425-114-70634

US-10-425-114-70634

US-10-751-235-17

US-10-751-235-16

US-10-751-235-16

US-10-751-235-16

US-10-751-235-16

US-10-751-235-16

US-10-282-1225-52999

US-10-282-1225-52999

US-10-282-1225-52999

US-10-282-1228-52999

US-10-751-235-37

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1867569 seqs, 417829326 residues
                                                                                                                                                                                                                                                                                                                US-10-751-235-10
122
1 LVAEVSEFLFGSGFAIAEGPLWTA 24
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                           OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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7737, Ap
27501, A
273682,
273682,
48081, A
1 48087, A
45724, A
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Sequence 1
Sequence 4
Sequence 2
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Sequence 3
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US-11-097-143-27501
US-10-424-599-273682
US-10-425-115-305171
US-10-282-122A-48087
US-10-369-493-10381
US-10-424-599-273679
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                                US-10-017-479-2
US-10-718-359-2
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Sequence 10, Application US/10751235

Sequence 10, Application US/10751235

Sequence 10, Application WS/20050150002A1

GENERAL INFORMATION:
APPLICANT: DellaPenna, Dean
APPLICANT: Tian, Li
APPLICANT: Tian, Joonyul
TILLE OF INVENTION: Novel Carotenoid Hydroxylases for Use in Engineering Carotenoid
TILLE OF INVENTION: Metabolism in Plants
FILE REFERENCE: MSU-086604
CURRENT APPLICATION NUMBER: US/10/751,235
CURRENT PILLING DATE: 2004-01-02
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin version 3.2
SEQ ID NO 10
LENGTH: 24
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100.0%; Score 122; DB 5;
Best Local Similarity 100.0%; Pred. No. 3.1e-12;
Matches 24; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTHER INFORMATION: Synthetic US-10-751-235-10
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1 LVAEVSEFLFGSGFAIAEGPLWTA 24

Sequence 265810, Application US/10424599
; Bequence 265810, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Acovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Zhou Yihua
; APPLICANT: Shou Yihua
; APPLICANT: Shou Yihua
; APPLICANT: Shou Yihua
; APPLICANT: Shou Yihua
; TITLE OF INVENTION: By Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFRENCE: 38-21(5322) B
; CURRENT APPLICATION NUMBER: US/10/424,599
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NOS: 285684
; TYPE: PRT US-10-424-599-265810

```
Sequence 18, Application US/10751235

Publication No. US20050150002A1

Publication No. US20050150002A1

GENERAL INFORMATION:
APPLICANT: DellaPenna, Dean
APPLICANT: Tan, Li
APPLICANT: Kim, Joonyul
TITLE OF INVENTION: Metabolism in Plants
TITLE OF INVENTION: Metabolism in Plants
FILE REFERENCE: MSU-08604
CURRENT APPLICATION NUMBER: US/10/751,235
CURRENT FILING DATE: 2004-01-02
NUMBER OF SEQ ID NOS: 74

SOFTWARE: Patentin version 3.2

SEQ ID NO 18

LENGTH: 362
                                                                                                                                       APPLICANT: Tian, Li
APPLICANT: Tian, Li
APPLICANT: Tian, Li
TITLE OF INVENTION: Novel Carotenoid Hydroxylases for Use in Engineering Carotenoid
TITLE OF INVENTION: Metabolism in Plants
FILE REPERENCE: MSU-08604
CURRENT APPLICATION NUMBER: US/10/751,235
CURRENT PILING DATE: 2004-01-02
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin version 3.2
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APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TILLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 114; DB 5; Length 208;
Pred. No. 6.6e-10;
0; Mismatches 1; Indels
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Publication No. US20040034888A1
GENERAL INFORMATION:
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                                        Sequence 21, Application US/10751235
Publication No. US20050150002A1
GENERAL INFORMATION:
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Best Local Similarity 95.8%;
Matches 23; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) ORGANISM: Triticum aestivum US-10-751-235-18
                                                                                                                                                                                                                                                                                                                                                                                                                                        ) ORGANISM: Helianthus annuus US-10-751-235-21
                                                                                                                     APPLICANT: DellaPenna, Dean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 22; Conserv
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                         8-10-751-235-21
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APPLICANT: Tian, Li
APPLICANT: Tian, Li
APPLICANT: Tian, Li
APPLICANT: Tian, Li
APPLICANT: Kim, Joonyul
TITLE OF INVENTION: Novel Carotenoid Hydroxylases for Use in Engineering Carotenoid
TITLE OF INVENTION: Metabolism in Plants
FILE REFERENCE: MSU-08604
CURRENT APPLICATION NUMBER: US/10/751,235
CURRENT FILING DATE: 2004-01-02
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
SEQ ID NO 4
LENGTH: 539
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APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
TITLE OF INVENTION: UNCLEIC AND USES THEREOF FOR PLANT IMPROVEMENT
TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-21(53377)B
CURRENT APPLICATION NUMBER: US/10/739,930
CURRENT PILING DATE: 2003-12-18
NUMBER OF SEQ ID NOS: 11088
SEQ ID NO 6317
LENGTH: 560
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                                                                                                                        Length 222;
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                                        ; OTHER INFORMATION: Clone ID: PAT_MRT3847_82046C.1.pep
US-10-424-599-265810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Clone ID: ARATH-23APR03-C3001_1.p
US-10-739-930-6317
                                                                                                                     Query Match
100.0%; Score 122; DB 4;
Best Local Similarity 100.0%; Pred. No. 3.7e-11;
Matches 24; Conservative 0; Mismatches 0;
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; Publication No. US20040216190A1
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/10751235
Publication No. US20050150002A1
GENERAL INFORMATION:
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ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Arabidopsis thaliana
US-10-751-235-4
ORGANISM: Glycine max FEATURE:
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Publication No. US20050150002A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Tian, Li
APPLICANT: Tian, Li
APPLICANT: Tian, Li
APPLICANT: Kim, Joonyul
TITLE OF INVENTION: Novel Carotenoid Hydroxylases for Use in Engineering Carotenoid
TITLE OF INVENTION: Metabolism in Plants
FILE REPERENCE: MGU-08604
CURRENT APPLICATION NUMBER: US/10/751,235
CURRENT PILING DATE: 2004-01-02
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin version 3.2
SEQ ID NO 16
LENGTH: 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 52, Application US/10751235
Publication No. US20050150002A1
GENERAL INFORMATION:
APPLICANT: DellaPenna, Dean
APPLICANT: Tian, Li
APPLICANT: Kim, Joonyul
TITLE OF INVENTION: Novel Carotenoid Hydroxylases for Use in Engineering Carotenoid
TITLE OF INVENTION: Metabolism in Plants
FILE REFERENCE: MSU-08604
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                                                                                                                                                                                                                                                                                              Gaps
                                TYPE: PRT

ROGANIEM: Hordeum vulgare

REATURE:

NAME/KEY: misc feature

LOCATION: (529)... (529)

COTHER INFORMATION: Xaa can be any naturally occurring amino acid

US-10-751-235-17
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                                                                                                                                                                                                                                      Query Match 90.2%; Score 110; DB 5; Length 545; Best Local Similarity 95.7%; Pred. No. 8.5e-09; Matches 22; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 110, DB 5; Length 56 Pred. No. 8.8e-09; 0; Mismatches 1; Indels
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CURRENT FILING DATE: 2004-01-02
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PATENTIN VERSION 3.2
                                                                                                                                                                                                                                                                                                                                                                              152 LVAEVSEFLFGSGFAIAEGALWT 174
                                                                                                                                                                                                                                                                                                                                                 1 LVAEVSEFLFGSGFAIAEGPLWT 23
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Best Local Similarity 95.7%;
Matches 22; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-751-235-16
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; ORGANISM: Oryza sativa
US-10-751-235-52
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LENGTH: 588
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APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 117686
LENGTH: 531
TYPP
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APPLICANT: Tian, Li
APPLICANT: Kim, Joonyul
TITLE OF INVENTION: Novel Carotenoid Hydroxylases for Use in Engineering Carotenoid
TITLE OF INVENTION: Movel Carotenoid Hydroxylases for Use in Engineering Carotenoid
TITLE OF INVENTION: NOVEL CARONISM IN Plants
FILE REFERENCE: MSU-08604
CURRENT APPLICATION NUMBER: US/10/751,235
CURRENT FILING DATE: 2004-01-02
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin version 3.2
SEQ ID NO 17
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Best Local Similarity 95.7%; Pred. No. 8.3e-09;
Matches 22; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                      OTHER INFORMATION: Clone ID: UC-ZMFLMO17009E12_FLI.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , OTHER INFORMATION: Clone ID: PAT_MRT4530_21069C.1.pep
US-10-437-963-117686
FILE REFERENCE: 38-21 (53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 70634
LENGTH: 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 117686, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       109 LVAEVSEFLFGSGPAIAEGDLWT 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 LVAEVSEFLFGSGFAIAEGPLWT 23
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Publication No. US20050150002A1
GRIERAL INFORMATION:
APPLICANT: DellaPenna, Dean
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                                                                                                                                                                                   ORGANISM: Zea mays
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US-10-751-235-17
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APPLICANT: XU, H.

APPLICANT: XU, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REPRENCE: ELITA.034

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT PILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/291,078

PRIOR PLILING DATE: 2000-05-23

PRIOR PLILING DATE: 2000-05-23

PRIOR PLILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/200,335

PRIOR PILING DATE: 2000-09-06

PRIOR PLILING DATE: 2000-09-06

PRIOR PLILING DATE: 2000-09-06

PRIOR PLILING DATE: 2000-10-23

PRIOR PLILING DATE: 2001-02-09

PRIOR PLILING DATE: 2001-02-09

PRIOR PLILING DATE: 2001-02-09

PRIOR PLILING DATE: 2001-02-09

PRIOR PLILING DATE: 2001-02-06

PRIOR PLILING DATE: 2001-02-16

PRIOR PLILING PLILING DATE: 2001-02-16

PRIOR PLILING PLILING DATE: 2001-02-16

PRIOR PLILING 
       PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SQCTWARE: Patentin version 3.1
SEQ ID NO 52949
LENGTH: 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 48.4%; Score 59; DB 4 Best Local Similarity 50.0%; Pred. No. 0.36; Matches 10; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 52999, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113 IIDEVTDIFIGMGFSIAEGP 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 LVAEVSEFLFGSGFAIAEGP 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRGANISM: Clostridium difficile US-10-282-122A-52949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Trawick, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T: Trawick, John
T: Carr, Grant
T: Yamamoto, Robert
T: Forsyth, R.
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                                                                                                                                                                                                                  Sequence 332853, Application US/10425115
; Publication No. US20040214272A1
; Publication No. US20040214272A1
; GENERAL INFORMATION:
GAPPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yongwal K.
APPLICANT: Cao, Yongwal K.
APPLICANT: Cao, Yongwal K.
APPLICANT: Can Yongwal K.
APPLICANT: Shou, Yihua
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 332853
LENGTH: 624
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TITLE OF INVENTION: 1dentification of Essential Genes in Microorganisms
FILE REPERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/203,335
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/230,347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Clone ID: MRT4577_66678C.1.pep
US-10-425-115-332853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: unsure
LOCATION: (1)..(624)
LOCATION: (1).. (624)
FEATURE:
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Sequence 52949, Application US/10282122A

Publication No. US20040029129A1

GENERAL INFORMATION:
APPLICANT: Wang, Liangsu

APPLICANT: Malone, Carlos

APPLICANT: Malone, Cheryl

APPLICANT: Haselbeck, Robert
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                                        1 LVAEVSEFLFGSGFAIAEGPLWT 23
1 LVAEVSEFLFGSGFAIAEGPLWT 23
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Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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US-10-425-115-332853
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APPLICANT:
APPLICANT:
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Sequence 244178

Sequence 244178

Sequence 241178, Application US/10425115

Publication No. US20040214272A1

SENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants

TITLE OF INVENTION: NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 244178

LENGTH: SO1

MANDER OF SED ID NOS: 369326
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                                                                                                                                                         0; Gaps
                                                                                                  Query Match
48.4%; Score 59; DB 4; Length 342;
Best Local Similarity 50.0%; Pred. No. 0.8;
Matches 10; Conservative 5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_154276C.1.pep
US-10-425-115-244178
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116 IIDEVTDIFIGMGFSIAEGP 135
                                                                                                                                                                                                      1 LVAEVSEFLFGSGFAIAEGP 20
; TYPE: PRT
; ORGANISM: Clostridium difficile
US-10-282-122A-52999
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Search completed: March 7, 2006, 22:04:14 Job time : 94.6 secs

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Score 58; DB 4; Length 501; Pred. No. 1.8; 7; Mismatches 6; Indels

Query Match
Best Local Similarity 40.9%;
Matches 9; Conservative

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Arabidops Arabidops Plant tra Thalecres Rice abio

Arabidops Arabidops

ADX66893 AAG17405 AAG17404 AAG16401

AAG16400 AD142851 AD003046 ABM87814

Mouse pre Arabidops Arabidops Plant pol Rice abio

Adx 66893 Aag17405 Aag17404 Aag16401 Aag16400 Add142851 Add142851 Abb79956 Abr 60146 A

AAE10987 ABB79956 ABR40828 ADT60146 ABM86366 ABG22889 AAG53830

Arabidops Arabidops Arabidops Arabidops Arabidops Plant (A.

AAU93039 ABB79954 ABB79955 ADB31801

Thalecres

# ALIGNMENTS

N-terminal peptide, SEQ ID NO: 11. tioxidant, transgenic plant; ESULT 1 EB16913

New expression vector comprising a nucleic acid sequence encoding a polypeptide having monooxygenase P450 activity, useful in altering the carotenoid production in a plant for enhancing production of specific carotenoid compounds.

Claim 8; SEQ ID NO 11; 135pp; English.

The present invention relates to genes, proteins and methods comprising carotenoid monooxygenases in the cytochrome P450 family. The invention also relates to altering carotenoid ratios in plants and microoxganisms using LUT1 epsilon-hydroxylases and/or CYP97A beta-hydroxylases. The invention is useful in altering the carotenoid production in a plant for enhancing production of specific carotenoid compounds that are potent antioxidants. The present sequence is thale cress chlorophyll-targeting N-terminal transit peptide.

) AEB16913 standard; peptide; 36 AA. ( arricola:		00-3EF-2003 (LILBC GILLLY)	3 Thale cress chloroplast-targeting N	Pigment; metabolic engineering; ant	ב ביינים	Arabidopsis thaliana.	1 US2005150002-A1.	07-JUL-2005.		02-JAN-2004; 2004US-00751235.	02-JAN-2004; 2004US-00751235.	(DELL/	(TIAN/) TIAN	Y (KIMU/) KIM U.	Dellapenna D, Tian L, Kim J;	WPI; 2005-487984/49.	New expression vector comprising a	polypeptide having monooxygenase	carotenoid production in a plant to		Claim 8; SEQ ID NO 11; 135pp; Engli	The present invention relates to ge	carotenoid monooxygenases	also relates to altering caroten	using LUT1 epsilon-hydroxylases	invention is useful in altering t	enhancing production of sp	antioxidants. The present sequence : -terminal transit peptide.		
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES

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Result	0100	Query	Concerb	2	F	Contraction
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1	177	100.0		σ	AEB16913	Aeb16913 Thale cre
7	177	100.0		0	AEB16908	Aeb16908 Thale cre
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4	75.5	42.7		٣	AAY44631	Aay44631 A. thalia
ß	75.5	42.7		4	AAB85456	Aab85456 Arabidops
9	63	35.6		æ	ADM48270	Adm48270 Polypepti
7	62.5	35.3	7	4	ABB63911	Abb63911 Drosophil
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0	9	33.9	355	2	ABB93995	Abb93995 Herbicida
10	9	33.9	389	٣	AAG54022	Aag54022 Arabidops
11	9	33.5	389	ო	AAG52506	
12	59.5	33.6	317	ო	AAG59958	Aag59958 Arabidops
13	59.5	33.6	317	m	AAG10212	Aag10212 Arabidops
14	59.5	33.6		m	AAG10211	•
15	59.5	33.6	319	ო	AAG59957	
16	59.5	33.6		ß	ABB93989	-
17	٥.	33.6		æ	ADT55654	Adt55654 Plant pol
18	29	•	<b>-т</b>	4	ABB65577	
19	57	32.2		m	AAG43792	Aag43792 Arabidops
20	26	31.6		4	ABG04863	Abg04863 Novel hum
21	26	31.6	407	٣	AAG22122	Aag22122 Arabidops
22	26	31.6	4	ო	AAG22121	Aag22121 Arabidops
23	26	31.6	474	æ	ADN74381	Adn74381 Thale cre
24	26	31.6	883	4	ABB62230	Abb62230 Drosophil

							RES ABI	X
GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd. OM protein - protein search, using sw model	March 7, 2006, 21:43:03; Search time 352.2 Seconds (without alignments) 44.911 Million cell updates/sec	US-10-751-235-11 BCOTE: 177 1 MESSLFSPSSSYSSLFTAKPTRLLSPKPKFTFSIR 36	table: BLOSUM62 Gapop 10.0 , Gapext 0.5	l: 2443163 segs, 439378781 residues	Total number of hits satisfying chosen parameters: 2443163	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	. A_Geneseq_21:*  1: geneseq_1990s:*  2: geneseq_1990s:*  3: geneseq_2000s:*  4: geneseq_2000s:*  5: geneseq_2001s:*  6: geneseq_2003s:*  7: geneseq_2003s:*  9: geneseq_2004s:*
OM prot	Run on:	Title: Perfect score: Sequence:	Scoring table:	Searched:	Total n	Minimum Maximum	Post-pr	Database

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Matches
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'note= "Chloroplast-targeting N-terminal transit peptide"
                                                                                                                                                                                                                                                                                                                                                          metabolic engineering; antioxidant; transgenic plant; CYP97C1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New expression vector comprising a nucleic acid sequence encoding a polypeptide having monooxygenase P450 activity, useful in altering the carotenoid production in a plant for enhancing production of specific
                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to 12005
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530. .531
/note= "Encoded by bases of positions 2340 to 2440"
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Misc-difference 165. 266

Misc-difference 255. 266

Misc-difference 332. 333
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                                                                                                                                                                                                                                                                                                                            Thale cress LUT1 (cytochrome P450 97C1) protein, SEQ ID NO: 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Encoded by bases of positions 1242 a 47. 352 /note= "Molecular oxygen binding pocket" 355. 366 /note= "Encoded by bases of positions 1420 a 480 a 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49. 450
note= "Encoded by bases of positions 1839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76. 477
note= "Encoded by bases of positions 2081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "Encoded by bases of positions 1662
                                   Length 36;
                                                                    Indels
                                                                                                    1 MESSLFSPSSSSYSSLFTAKPTRLLSPKDKFTFSIR 36
                                   Score 177; DB 9;
Pred. No. 1.9e-17;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                            AEB16908 standard; protein; 539 AA
                                 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-JAN-2004; 2004US-00751235.
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                                                                                                                                                                                                                                                                                             (first entry)
                                                      Best Local Similarity 100 Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tian L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DELL/) DELLAPENNA D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  compounds
                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana.
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                                                                                                                                                                                                                                                                                                                                                                              cytochrome P450 97C1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
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                                                                                                                                                                                                                                                                                              08-SEP-2005
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     Sequence 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  carotenoid
                                                                                                                                                                                                                                                             AEB16908;
                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                Pigment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Region
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Claim 9; SEQ ID NO 4; 135pp; English.

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The invention relates a recombinant DNA construct comprising a polymucleotide having any of 5544 nucleotide sequences (CDNAs SEQ ID NO: 15544) and encoding a polypeptide with any of 5544 amino acid sequences (SED ID NO: 5545-11088). The CDNAs and proteins are from corn, soybean, Arabidopsis, wheat and rape but the specification does not indicate which sequences is derived from which organism. Also included is a method of producing a plant having an improved property, comprising transforming a plant with a recombinant DNA construct comprising a promoter region functional in a plant cell operably joined to a polynucleotide encoding a polypeptide associated with the property, and growing the transformed plant. The property is selected from improving plant cold tolerance, for manipulating growth rate in plant cells by modification of the cell cycle
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The present invention relates to genes, proteins and methods comprising carotenoid monooxygenases in the cytochrome P450 family. The invention also relates to altering carotenoid ratios in plants and microorganisms using LUT1 epsilon-hydroxylases and/or CYP97A beta-hydroxylases. The invention is useful in altering the carotenoid production in a plant for enhancing production of specific carotenoid compounds that are potent antioxidants. The present sequence is thale cress LUT1 [cytochrome P450 monooxygenase (CYP97C1); AL5951310 genel protein. Note: The current sequence is that of thale cress LUT1 protein that is encoded by cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    plant; transgenic; cold tolerance; growth rate; drought tolerance; disease resistance; galactomannan production; plant growth regulator; heat tolerance; herbicide tolerance; lignin production; extreme osmotic condition tolerance; pathogens resistance; pest resistance; yield improvement; seed oil yield; seed protein yield.
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100.0%; Pred. No. 4.5e-16;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MESSLFSPSSSSYSSLFTAKPTRLLSPKPKFTFSIR
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28-APR-2003; 2003US-00425115.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                       located on chromosome 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 539 AA;
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co pathway, for improving plant drought tolerance, for providing increased resistance to plant disease, for galactomannan production, for production of plant growth regulators, for improving plant heat tolerance. for improving plant tolerance to herbicides, for increasing the rate of homologous recombination in plants, for lignin production, for improving plant tolerance to extreme osmotic conditions, for improving plant tolerance to pathogens or peets, for yield improvement by modification of photosynthesis, for modifying seed oil yield and/or content, for modification of carbohydrate, nitrogen or phosphorus use and/or uptake and for yield improvement by providing improved plant growth and modification of carbohydrate, nitrogen or phosphorus use and/or uptake and for yield improvement by providing improved plant growth and evelopment under at least one stress condition. The polymiclectide may also encode a plant transcription factor. The methods and compositions of the present invention are useful in the field of biochemistry and compositions also encode a plant transcription factor. The methods and compositions of the present invention are useful in the field of biochemistry and biological characteristics such as increased yield, improved nitrogen biological characteristics such as increased plants with improved biological characteristics such as increased storing plant tolerance to cold or heat, improving plant tolerance to extreme osmotic and drought conditions, and improving plant colerance to plant psets or pathogens. They can also be used in physical arrays of molecules, plant breeding markers, computer-based storage and analysis systems. The present sequence is one of the 5544 plant protein cold cord cord or cord or conditions of the invention. Note: The sequence data for this patent did electronic format directly from USPND at sequence of the printed specification, but was obtained in electronic format directly from USPND at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 177; DB 8; Length 560; 100.0%; Pred. No. 4.7e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5'-phosphoribosyl-5-aminoimidazole synthetase; weed growth; purine biosynthesis; recombinant AIR synthetase; herbicide.
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(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.

    A. thaliana AIR synthetase pre-protein.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 560 AA;
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Matches
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New isolated enzyme with phosphoribosyl-5-aminoimidazole synthetase activity, used to screen for herbicides or to produce herbicide-tolerant

N-PSDB; AAZ49679

Claim 3; Page 53-54; 58pp; English

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated nucleic acid encoding a S'-phosphoribosyl-5-aminoimidazole synthase, used to transform plant cells, for use in screening for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              synthetase from Arabidopsis. The AIR synthetase protein can be expressed by standard recombinant methodology. Nucleic acids encoding the AIR synthetase are used for producing transgenic plants and plant cells, for screening herbicidal compounds which inhibit the enzymatic activity of AIR synthetase. The present sequence represents an Arabidopsis AIR synthetase sequence
          The present sequence is A. thaliana AIR (5'-phosphoribosyl-5--
aminoindazole) synthetese pre-protein, an enzyme involved in de novo
purine biosynthesis. The cDNA is deposited in E. coli strain DifsapASM
designated as NRRL accession number B-21976. Recombinantly produced AIR
synthetese enzyme can be used in screening chemicals for herbicidal
activity. Plants having modified enzyme activity are tolerant to
inhibition by herbicides. Herbicide-tolerant AIR synthetase is also
                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                       Indels 3;
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                                                                                                                                                                           DB 3; Length 386;
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0.063;
10;
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0.063;
10;
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                                                                                                                                                                                                                                                     1 MEARILOSSSCYSSLYTVNRSRFSSPKP---FSV 32
                                                                                                                                                                                                                                    1 MESSLFSPSSSSYSSLFTAKPTRLLSPKPKFTFSI 35
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                                                                                                                                                                        Score 75.5; DB
Pred. No. 0.063;
5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis, transgenic; herbicide; enzyme.
                                                                                                                  useful as a selectable marker in plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SYGN ) SYNGENTA PARTICIPATIONS AG.
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                                                                                                                                                                                                                                                                                                                                          AAB85456 standard; protein; 386
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                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis AIR synthetase
                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                      Query Match
Best Local Similarity 48.6
Matches 17; Conservative
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Matches 17; Conservative
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                                                                                                                                               Sequence 386 AA;
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                                                                                                                                                                                                                                                                                                            RESULT 5
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The present invention relates to polymucleotide sequences, and the proteins they encode. The sequences are isolated from a variety of organizams unto as plants (e.g. maize, rice, sorghum, thale cress, corgonal and wheat), cyanobacteria, bacteria, yeast and other fungi. The polymucleotide and polypeptide sequences of the invention are useful in the production of transgenic plants that have improved properties. Also disclosed are methods of producing fertile transgenic plants, preferably maize, with desired phenotypes. The polymucleotide and polypeptide sequences are useful for improving plants by providing protection against sequences are useful for improving plants by providing protection against modifying the cell cycle pathway, reducing plant height, modifying carbohydrate transport, improving crop productivity, improving plant growth and stress resistance, improving disease resistance, improving plant assimilation, improving stalk strength, improving native and ablotic and absorbed in the control of improving plant assimilation, improving stalk strength, improving and absorbed in a subject of improving plants of improving pla
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                                                                                                                                                                                                                                                                                                                                                               plant; maize; rice; sorghum; thale cress; soybean; wheat; transgenic; osmotic stress; sugar transport; cell cycle pathway; plant height; carbohydrate transport; crop productivity; plant growth; stress resistance; disease resistance; insect resistance; heat tolerance; nitrogen assimilation; water stress tolerance; photosynthetic carbon fixation; virus resistance; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polynuclectide, useful for manipulating plant protein quality, improving plant growth, yield and crop productivity or grain composition or producing plants with improved properties.
                                                                                                                                                                                                                                                                                                             Polypeptide sequence #320 useful in producing transgenic plants.
1 MEARILQSSSSCYSSLYTVNRSRFSSPKP---FSV 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 8; SEQ ID NO 688; 144pp; English.
                                                                                                                                       ADM48270 standard; protein; 260 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-DEC-2001; 2001US-0337358P.
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                                                                                                                                                                                                                                                        (first entry)
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Best Local Similarity 46.2
Matches 12; Conservative
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CHOMET P S.
LACCETTI L B.
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                                                                                                                                                                                                                                                        03-JUN-2004
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                                                                                        RESULT
                                                                                                                   ADM4827
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Laccetti LB;

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-ABB72072). The sequence data for this patent did not form part of printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                 Drosophila, developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 18525; 21pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 62.5; DB 4; Length 2
Pred. No. 30;
4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   986 SSLFSPSQVDSTSSLFAPPPTSANTTILTPAPDTTSTL 1023
                                                                                                                                                                                              Drosophila melanogaster polypeptide SEQ ID NO 18525.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Myers EW;
10 SSSYSSLFTAKPTRLLSPKPKFTFSI 35
                 4 SATSASLFSANPTPLFSPKPSLSLHL 29
                                                                                                          ABB63911 standard; protein; 2016 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 35.3%;
Best Local Similarity 47.4%;
Matches 18; Conservative 4
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11-JUL-2000; 2000US-00614150.
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                                                                                                                                                                      26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                  Drosophila melanogaster.
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                                                                                                                                                                                                                                                   pharmaceutical
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Score 63; DB 8; Length 260; Pred. No. 2.3; 6; Mismatches 8; Indels

35.6%;

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9905-0148341P
9905-014855P
9905-0149368P
9905-0149175P
9905-0149722P
9905-0149722P
9905-0149723P
9905-0149902P
9905-0149902P
9905-0150868P
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  99US-0139899P.
99US-0140353P.
99US-0140695P.
99US-014083P.
99US-0140991P.
99US-0141842P.
99US-014287P.
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99US-0144332P.
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99US-0144352P.
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99US-0144814P.
99US-0145086P.
99US-0145088P.
                                        24-JUN-1999;
28-JUN-1999;
29-JUN-1999;
30-JUN-1999;
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                         Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay. genetic mapping; gene expression control; promoter; termination sequence.
Arabidopsis thaliana protein fragment SEQ ID NO: 31259
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99US-0123180P.
99US-0125368P.
99US-0126264P.
99US-0126785P.
99US-0127462P.
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9905-0129845P
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9905-013248P
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9905-01324807P
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99US-0138094P.
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99US-0136021P.
99US-0136392P.
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                                                                             Arabidopsis thaliana
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                                                                                                                                                           sednences
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                            Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequenc from plant with nucleic acid or amino acid sequences from non-plant
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                                                                                                                                                                                                                           Claim 5; SEQ ID NO 3206; 261pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                         33.9%; Score 60; DB 5; Length 355; 42.1%; Pred. No. 8.7; tive 6; Mismatches 10; Indels
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99US-0123180P.
99US-012548P.
99US-0125788P.
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99US-0127462P.
99US-0127462P.
99US-0128234P.
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                                  28-AUG-2001; 2001WO-EP009892
                                                            28-AUG-2001; 2001WO-EP009892
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                               Tietjen K, Weidler M;
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Best Local Similarity
                                                                                       (FARB ) BAYER AG
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 355 AA;
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25-MAR-1999;
29-MAR-1999;
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05-MAR-1999;
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            07-FEB-2002
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                                                                                                                                         9908-0156659F
9908-0156458P
9908-0157117P
9908-0157731P
9908-0157638P
9908-0158858P
9908-015828P
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9905-0160767P.
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9905-0160980P.
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99US-0159637P.
99US-0159538P.
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99US-0161359P.
99US-0161360P.
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99US-0155139P.
99US-0155486P.
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99US-0162142P
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Best Local Similarity 40.0
Matches 14; Conservative
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13-0CT-1999;
13-0CT-1999;
14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
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                                                  10.SEP-1999;
13.SEP-1999;
16.SEP-1999;
20.SEP-1999;
22.SEP-1999;
23.SEP-1999;
24.SEP-1999;
24.SEP-1999;
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05-OCT-1999;
06-OCT-1999;
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22-OCT-1999;
22-OCT-1999;
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21-OCT-1999
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01-APR-1999; 06-APR-1999; 08-APR-1999; 16-APR-1999;

Arabidopsis thaliana. WO200210210-A2

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                                                                                                                                                                                          17-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                       Arabidopsis thaliana
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03-JUN-1999;
04-JUN-1999;
  28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
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25-MAR-1999;
29-MAR-1999;
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14-MAY-1999;
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us-10-751-235-11.rai

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MOLECULE TYPE: protein
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Sequence 21929, A
Sequence 21929, A
Sequence 244, Appl
Sequence 34, Appl
Sequence 34, Appl
Sequence 34, Appl
Sequence 69, Appl
Sequence 61, Appli
Sequence 1, Appli
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Sequence 35788, A
Sequence 51005, A
Sequence 9153, Ap
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                                                                                    March 7, 2006, 21:58:31; Search time 40.2 Seconds (without alignments) 74.038 Million cell updates/sec
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Sequence 2,
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GenCore version 5.1.7
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, APE	APPLICANT:	Subram	Subramanian, Walters Eric	Mani	ņ			
LIT.	TITLE OF INVENTION:	VENTION	7: Methods	hod	s to screen herbicidal		compounds	
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·- ·-	OPERATING SYSTEM:	SYSTEM	•	ac. D0S				
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4	APPLICATION NUMBER:	ON NUMB	BER: 0	09/103	03,895			
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	NAME: St	Stults, Larry W	arry W					
, r.	REGISTRATION NUMBER:	NOI NOI	BER:	34,025	025			
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r.	TELEPHONE:	3: 919-	919-541-8666	99				
,	TELEFAX:	-	919-541-8689					
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Gaps

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Score 75.5; DB 2; Length 386; Pred. No. 0.017; 5; Mismatches 10; Indels

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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANG

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1999-02-12

PRIOR PILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 23978

LENGTH: 117
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US-09-248-796A-21929

US-09-248-796A-21929

Sequence 21929, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: PCR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: PCR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: PCR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US 60/0744,725

PRIOR APPLICATION NUMBER: US 60/0744,725

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-08-13

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 ESSLF-----SPSSSSYSSLFTAK-----PTRLLSPKPKFT 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 SSLFSPSSSSYSSL-FTAKPTRLL----SPKPKFTFSI 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25 SFLSQQHSSKYSYIHFTMIPTRILLINGAKNVKPKLTYPV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 244, Application US/09487558B Patent No. 6949356 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 30.2%;
Best Local Similarity 34.1%;
Matches 15; Conservative 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 41.0%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Maxon, Mary
Milne, Todd
No. 6949356man, '
Royer, John
                                                                                                                                                                                                                                                                                                                                                                           , ORGANISM: Candida albicans
US-09-248-796A-23978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Candida albicans
US-09-248-796A-21929
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Holtzman, Doug
Madden, Kevin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Busby, Robert APPLICANT: Cali, Brian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-487-558B-244
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: LAGARIAS, JOHN
APPLICANT: ACCITH, TARAVUTI
APPLICANT: RANKENBERG, NICOLE
APPLICANT: GAMBETTA, GREGORY
APPLICANT: GAMBETTA, GREGORY
APPLICANT: MANYGOMERY: BERONDA
TITLE OF INVENTION: LIGHT CONTROLLED GENE EXPRESSION UTILIZING HETEROLOGOUS PHYTOCHRG
FILE REPERENCE: 407T-907731US
CURRENT APPLICATION NUMBER: US/10/159,901
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: 60/294,463
PRIOR FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 57
SOFTWARE: Patentin Version 3.0
SEQ ID NO 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Kelth Weinstock et al
APPLICANTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT PAPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-13
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION WUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
PRIOR FILING DATE: 1998-08-13
SRO ID NO 21631
LENGTH: 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 54.5; DB 2; Length 1
Pred. No. 5.1;
6; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 SKKISPSLSSITTTTAEDESINDLPTNVITPTPKTT 53
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                                      1 MEARILQSSSCYSSLYTVNRSRFSSPKP---FSV 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 21631, Application US/09248796A Patent No. 6747137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-248-796A-23978
; Sequence 23978, Application US/09248796A
                                                                                                                                                                              Sequence 57, Application US/10159901; Patent No. 6887688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Arapidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30.8%;
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Best Local Similarity 37.89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Candida albicans
US-09-248-796A-21631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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GENERAL INFORMATION:
APPLICANT: UNITED STATES OF AMERICA; DEFT.
APPLICANT: UNITED STATES OF AMERICA; DEFT.
APPLICANT: OF HEALTH AND HUMAN SERVICES
TITLE OF INVENTION: MOTILITY STIMULATING
TITLE OF INVENTION: THERAPY
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 29.9%; Score 53; DB 1; Length 829; Best Local Similarity 48.0%; Pred. No. 59; Matches 12; Conservative 3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION:
IDENTIFICATION METHOD:
CHER INFORMATION: Putative protein
OTHER INFORMATION: Requence of A2058 Autotaxin
US-08-346-455B-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              235 FGPEESSYGSPFTPAKRPKRKVAPK 259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA: .
APPLICATION NUMBER: US/08/977,221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/346,455
FILING DATE: 28-NOV-1994
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/249,182
FILING DATE: 25-MAY-1994
PRIOR APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: Floppy Disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WordPerface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 34, Application US/08977221 Patent No. 6084069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36,434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER
               STRANDEDNESS: Single TOPOLOGY: Unknown MOLECULE TYPE: protein HYPOTHETICAL: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                          HAPLOTYPE:
TISSUB TYPE:
CELL TYPE: Melanoma
CELL LINE: A2058
ORGANELLE:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                         INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: NEW YORK STATE: NEW YORK COUNTRY: U.S.A.
                                                                                                                                               ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10154
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                                                                                                                                                                      STRAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                            APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.130
CURRENT APPLICATION NUMBER: US/09/487,558B
CURRENT FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/487,558
PRIOR PLINING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 446
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 34, Application US/08346455B

Patent No. 5731167

GENERAL INFORMATION:

APPLICANT: UNITED STATES OF AMERICA; DEPT.

APPLICANT: UNITED STATES OF AMERICA; DEPT.

APPLICANT: UNITED STATES OF AMERICA; DEPT.

APPLICANT: UNITED STATES OF AMERICA; TITLE OF INVENTION: MOTILITY STIMULATING

TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND

TITLE OF INVENTION: THERAPY

NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN

STREET: 345 PARK AVENUE

CITY: NEW YORK

CITY: NEW YORK

CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1564;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 53.5; DB 2;
Pred. No. 1.1e+02;
9; Mismatches 8;
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612 SLYRPSADAFASTFSDVPTKLAT---AVTFNI 640
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MEDIUM TYPE: Floppy Digk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346,455B
FILING DATE: 28-NOV-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06613
FILING DATE: 24-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06613
FILING DATE: 25-MAY-1994
PROR APPLICATION DATA:
APPLICATION NUMBER: 08/349,182
FILING DATE: 17-JAN-1994
RECOMPANY TROUGHTON TO THE APPLICATION NUMBER: 08/349,182
FILING DATE: 17-JAN-1995
ATTORNEY AGENT INFORMATION:
ANAME: COOCHELY DATE: 17-JAN-1992
ATTORNEY AGENT INFORMATION:
ANAME: COOCHELY DATE: APPLICATION NUMBER: 07-JAN-1992
                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-487-558B-244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 20.
IELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (212) 758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 30.2%;
Best Local Similarity 37.5%;
Matches 12; Conservative
                                            Silva, Jeff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NEW YORK
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                                                                                                                                                                                                                                                                                               SEQ ID NO 244
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APPLICANT: STRACKS, MARY; LIOTTA, LANCE;
APPLICANT: SCHIFFRANN, ELLIOTT; KRUTZSCH,
APPLICANT: HENRY; MURATA, JUN
APPLICANT: HENRY; MURATA, JUN
TITLE OF INVENTION: MOTILITY STIMULATING
TITLE OF INVENTION: THERAPY
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
COUNTRY: U.S.A.
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: PLORY:
COMPUTER READABLE FORM:
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TISSUE TYPE:
TISSUE TYPE:
CELL TYPE: Melanoma
CELL TYPE: A2058
ORGANELE:
PRATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: Sequence of A2058 Autotaxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC COMPACTIBLE
COMPUTER: IBM PC COMPACTIBLE
COMPUTER: IBM PC COMPACTIBLE
COMPUTER: IBM PC COMPACTIBLE
SOFTWARE: Wordberfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06613
FILING DATE: 24-MAY-1995
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/346,455
FILING DATE: 28-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 00/249,182
FILING DATE: 25-MAY-1994
PRIOR APPLICATION NUMBER: 07/82,043
FILING DATE: 17-JAN-1992
ATPONEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
                                                                                                                                                              235 PGPEESSYGSPFTPAKRPKKVAPK 259
                                                                                                                                                                                                                                                                                                                            CT-US95-06613-34
Sequence 34, Application PC/TUS9506613
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
HYPOTHETICAL: No
ORIGINAL SOURCE:
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE
                                                                                                                                                         g
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| GENERAL INFORMATION: |
| APPLICANT: STRACKE, MARY |
| APPLICANT: STRACKE, HENRY |
| APPLICANT: KRUTZCH, HENRY |
| APPLICANT: KRUTZCH, HENRY |
| APPLICANT: MUNEATA, JUN |
| TITLE OF INVENTION: CANCER DIAGNOSIS AND THERAPY |
| TITLE OF INVENTION: CANCER DIAGNOSIS AND THERAPY |
| TITLE OF INVENTION: CANCER DIAGNOSIS AND THERAPY |
| TITLE OF INVENTION: CANCER DIAGNOSIS AND THERAPY |
| TITLE OF INVENTION: CANCER DIAGNOSIS AND THERAPY |
| TITLE OF INVENTION NUMBER: US/09/483,831B |
| CURRENT FILING DATE: 1992-01-17 |
| PRIOR FILING DATE: 1994-05-25 |
| PRIOR FILING DATE: 1994-11-28 |
| PRIOR FILING DATE: 1994-11-24 |
| NUMBER OF SEQ ID NOS: 70 |
| SEQ ID NO 34 |
| LANCH: 829 |
| LANCH: BASPELICATION NUMBER: OR/377,221 |
| LEMOTH: 829 |
| LANCH: BASPELICATION NUMBER: OR/377,221 |
| LANCH: BASPELICATION NUMBER: OR/377,221 |
| LEMOTH: 829 |
| LANCH: BASPELICATION NUMBER: OR/377,221 |
| LEMOTH: BASPELICATION NUMBER: OR/370 |
| LEMOTH: OR/370 |
| LEMOTH: OR/370 |
| LEMOTH: OR/370 |
| LEMOTH: OR/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , OTHER INFORMATION: Putative protein sequence of A2058 Autotoxin
US-09-483-831B-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 29.9%; Score 53; DB 2; Length 829; Best Local Similarity 48.0%; Pred. No. 59; Matches 12; Conservative 3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 29.9%; Score 53; DB 2; Length 829; Best Local Similarity 48.0%; Pred. No. 59; Matches 12; Conservative 3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: Putative protein
OTHER INFORMATION: sequence of A2058 Autotaxin
US-08-977-221-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                235 FGPEESSYGSPFTPAKRPKRKVAPK 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 FSPSSSSYSSLFT--AKPTRLLSPK 28
TELEFAX: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 829
TYPF:
                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDENNESS: single
TOPOLOGY: Unknown
MOLECULE TYPE: protein
HYPOTHETICAL: No
                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE:
ORGANISM: Human
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Melanoma
CELL TYPE: Melanoma
ORGANELLE:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 9
US-09-483-831B-34
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Sequence 69, Application US/08977221
Patent No. 6084069
GENERAL INFORMATION:
APPLICANT: UNITED STATES OF AMERICA, DEPT.
APPLICANT: OF HEALTH AND HUMAN SERVICES
TITLE OF INVENTION: MOTILITY STIMULATING
TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
TITLE OF INVENTION: THERAPY
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 915;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/346,455
FILING DATE: 28-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,182
FILING DATE: 25-MAY-1994
PRIOR APPLICATION NUMBER: 07/822,043
APPLICATION NUMBER: 07/822,043
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
RECENENCE/DOCKET NUMBER: 2026-4149US3
TELEFHONE: (212) 75-4800
TELEFHONE: (212) 75-6849
INPORMATION FOR SEQ ID NO: 69:
SEQUENCE: CLARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

29.9%; Score 53; DB
Best Local Similarity 48.0%; Pred. No. 67;
Matches 12; Conservative 3; Mismatches
                                                     321 FGPEESSYGSPFTPAKRPKRKVAPK 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       321 FGPEESSYGSPFTPAKRPKRKVAPK 345
  6 FSPSSSSYSSLFT--AKPTRLLSPK 28
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/977,221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: MORGAN & FINNEGAN STREET: 345 PARK AVENUE CITY: NEW YORK COUNTRY: U.S.A. ZIP: 10154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: A2058 ATX protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IDENTIFICATION METHOD:
CTHER INFORMATION:
US-08-977-221-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: CI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
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                                                                                                                                                                                                                                                                                                                                         29.9%; Score 53; DB 1; Length 915; 48.0%; Pred. No. 67; tive 3; Mismatches 8; Indels
                                                          DB 4; Length 829;
                                                       ; Score 53; DB 4; Pred. No. 59; 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: NEW YORK
COUNTRY: NEW YORK
COUNTRY: U.S.A.
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: TAM FC compatible
COMPUTER: TAM FC COMPATION
NAME: DOROTHY R. AUTH
RECISTRATION NUMBER: TAM FC COMPATION
NAME: DOROTHY R. AUTH
RECISTRATION NUMBER: TO 78 - 4800
TELEPONE: (212) 75 - 6849
INFORMATION FOR SEQ ID NO: 69:
SENTENCE COMPATICES:
COMPUTER: COMPATICES:
COMPUTER: COMPATICES:
COMPUTER: COMPATICES:
COMPUTER: TAM FC COMPATICES:
COMPUTER: CO
                                                                                                                                                                                                        235 FGPEESSYGSPFTPAKRPKKVAPK 259
                                                                                                                                                                    6 PSPSSSSYSSLFT--AKPTRLLSPK 28
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                                                     Query Match 29.9%;
Best Local Similarity 48.0%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   345 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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IDENTIFICATION METHOD:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single COPOLOGY: Unknown AECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 12; Conserva
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                                                                                                                                                                                                                                                                                                                                       US-08-346-455B-69
PCT-US95-06613-34
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Search completed: March 7, 2006, 22:00:14 Job time : 40.2 secs
FILING DATE: 25-MAY-1994
RIGHT PAPLICATION DATA:
APPLICATION NUMBER: 07/822.042
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION:
1 IDENTIFICATION METHOD:
1 OTHER INFORMATION:
PCT-US95-06613-69
                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: Unkno
MOLECULE TYPE: CI
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-914-272A-1
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                                                                          FACENTE NO. 541/39 HERRAL INFORMATION:
APPLICANT: STRACKE, MARY
APPLICANT: ALOTTA, LANCE
APPLICANT: SCHIFFMANN, ELLIOTT
APPLICANT: SCHIFFMANN, ELLIOTT
APPLICANT: KRUTZCH, HENRY
APPLICANT: KRUTZCH, HENRY
APPLICANT: MURATA, JUN
TITLE OF INVENTION: CANCER DIAGNOSIS AND THERAPY
FILE REPRENCE: 2026-4149084
CURRENT APPLICATION NUMBER: US/09/483,831B
CURRENT FILING DATE: 1992-01-17
PRIOR APPLICATION NUMBER: 07/822,043
FRIOR FILING DATE: 1994-05-25
FRIOR FILING DATE: 1994-11-28
FRIOR FILING DATE: 1994-11-28
FRIOR FILING DATE: 1994-11-24
FRIOR RELING DATE: 1994-11-24
FRIOR FILING DATE: 1994-11-24
FRIOR FILING DATE: 1994-11-24
FRIOR FILING DATE: 1994-11-24
FRIOR FILING DATE: 1997-11-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: STRACKE, MARY; LIOTTA, LANCE;
APPLICANT: SCHIFFMANN, ELLIOTT; KRUTZSCH,
APPLICANT: HENRY; MURATA, UN
TITLE OF INVENTION: MOTILITY STIMULATING
TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
TITLE OF INVENTION: THERAPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 915;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 29.9%; Score 53; DB 2; Best Local Similarity 48.0%; Pred. No. 67; Matches 12; Conservative 3; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          321 FGPEESSYGSPFTPAKRPKRVAPK 345
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FILING DATE: 24-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 FSPSSSSYSSLFT--AKPTRLLSPK 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDERTECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 69, Application PC/TUS9506613 GENERAL INFORMATION:
                                        Sequence 69, Application US/09483831B Patent No. 6417338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/346,455
FILING DATE: 28-NOV-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
PCT-US95-06613-69
                   US-09-483-831B-69
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67;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SARGUCHI, NO. 6673913uo
APPLICANT: SURGABATA KARUHIKO
TITLE OF INVENTION: GANP Protein
FILE REPERRNCE: 050208-0014
CURRENT APPLICATION NUMBER: 105/914,272A
CURRENT FILING DATE: 2001-08-24
PRIOR FILING DATE: 1999-08-27
PRIOR FILING DATE: 1999-08-27
PRIOR FILING DATE: 1999-08-27
PRIOR FILING DATE: 1999-08-27
NUMBER OF SEQ ID NOS: 9
APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
FELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEPHONE: (212) 758-4800
TELEPAX: (212) 751-6849
INFORMATION FOR SEC ID NO: 69:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 29.9%; Score 53; DB Best Local Similarity 48.0%; Pred. No. 67; Matches 12; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  321 FGPEESSYGSPFTPAKRPKRKVAPK 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 FSPSSSSYSSLFT--AKPTRLLSPK 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09914272A Patent No. 6673913
                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: A2058 ATX protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 1971
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GenCore version 5.1.7
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protein search, using sw model OM protein Run on:

March 7, 2006, 22:00:32 ; Search time 15.6 Seconds (without alignments) 46.155 Million cell updates/sec

US-10-751-235-11

Title: Perfect score:

1 MESSLPSPSSSSYSSLPTAKPTRLLSPKPKFTFSIR 36 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

135346 seqs, 20000420 residues Searched:

Total number of hits satisfying chosen parameters:

135346

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published Applications AA New:\*

(cgn2\_6/ptodata/1/pubpa4/USO8\_NEW\_PUB.pep:\*

(cgn2\_6/ptodata/1/pubpaa/USO6\_NEW\_PUB.pep:\*

(cgn2\_6/ptodata/1/pubpaa/USO7\_NEW\_PUB.pep:\*

(cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*

(cgn2\_6/ptodata/1/pubpaa/NSO3\_NEW\_PUB.pep:\*

(cgn2\_6/ptodata/1/pubpaa/USO3\_NEW\_PUB.pep:\*

(cgn2\_6/ptodata/1/pubpaa/USI0\_NEW\_PUB.pep:\*) Database :

/cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\* /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 4, Appli	~	Sequence 1, Appli	63	-	44	52,	73,	3586	Sequence 5, Appli	7	164	246	Sequence 124, App	1199	Sequence 1126, Ap	446,	238	3028,	101	314	20,	126		6
SUMMAKIES	ID	US-10-838-616-4	US-11-094-586-2	US-11-179-624-1	US-11-087-099-6346	US-10-877-346-44	US-11-240-341-44	US-10-517-939-52		US-11-072-512-3588	US-10-514-531-5	US-10-514-531-2	US-10-793-626-164	7	US-11-165-226-124		US-10-821-234-1126 .	US-11-124-367A-446	US-10-714-887-238	US-11-072-512-3028	7	US-11-033-039-314	US-10-915-161-20	US-10-524-647-126	US-10-524-972-114	US-10-915-161-2
	DB	9	7	7	7	9	7	9	^	7	9	9	9	7	^	7	9	^	9	7	9	7	9	ø	9	9
	Query Match Length	352	639	1971	505	1905	527	1053	1142	312	797	798	130	161	688	906	1199	1972	199	285	680	1890	120	366	366	265
de	Query Match	29.9	29.9	29.9	27.4	27.4	27.1	27.1	27.1	26.8	26.8	26.8	26.6	26.6	26.6	26.6	26.6	26.6	26.3	26.3	26.3	26.0	25.4	25.4	25.4	25.4
	Score	53	53	23	48.5	48.5	48	48	48	47.5	47.5	47.5	47	47	47	47	47	47	46.5	ė.	46.5	46	45	45	45	45
	Result No.	-	7	٣	4	S	9	7	œ	0	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Sequence 2246, Ap Sequence 52, Appl	Sequence 10, Appl Sequence 16, Appl	Seguence 1543, Ap	40,	Sequence 38, Appl	Seguence 32, Appl	Sequence 30, Appl	Sequence 36, Appl	Sequence 34, Appl	Sequence 28, Appl	Sequence 26, Appl	Sequence 324, App	Sequence 19, Appl	Sequence 2, Appli	Sequence 627, App	Seguence 331, App	Sequence 2898, Ap
US-11-072-512-2246 US-11-113-424-52	US-11-100-640-10 US-11-100-640-16	US-10-821-234-1543	US-11-114-906-40	US-11-114-906-38	US-11-114-906-32	US-11-114-906-30	US-11-114-906-36	US-11-114-906-34	US-11-114-906-28	US-11-114-906-26	US-11-024-959-324	US-11-182-016-19	US-11-134-563-2	US-10-330-773-627	US-11-207-078-331	US-10-793-626-2898
3 7 5	<u>ر</u> ر	9 1	7	7	7	7	7	7	7		7	7	7	9	1 7	9
723	272	71	838	851	98	87	95	95	976	98	102	173	38	234	7	108
25.4	25.4	25.1	25.1	25.1	25.1	25.1	25.1	25.1	25.1	25.1	25.1	25.1	24.9	24.9	24.6	24.6
4.5 7.4 7.5	4 5 5	44.5	44.5	44.5	44.5	44.5	44.5	44.5	44.5	44.5	44.5	44.5	44	44	43.5	43.5
26 27	2 2 3 3	30	32	33	34	. 35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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APPLICANT: Mendel Blotechnology, Inc.
APPLICANT: Mendel Blotechnology, Inc.
APPLICANT: CREELMAN, Robert A
APPLICANT: RATCLIFFE, Oliver
APPLICANT: GUTTERSON, Neal I
APPLICANT: GUTTERSON, Neal I
APPLICANT: GUTTERSON, Neal I
APPLICANT: LIBBY, Jeffrey M
TITLE OF INVENTION: Plant Transcriptional Regulators of Abiotic Stress
FILE OF INVENTION: Plant Transcriptional Regulators of Abiotic CURRENT APPLICATION NUMBER: 105/10/838,616
CURRENT FILING DATE: 2004-05-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 68
SOFTWARE: PatentIn version 3.2
SEQ ID NO 4
LENGTH: 352
                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT FILING DATE: 2004-05-04

PRIOR APPLICATION NUMBER: Stress-Related Polypeptides in Plants
PRIOR FILING DATE: 2004-05-04

PRIOR FILING DATE: 2004-04-26

PRIOR FILING DATE: 2003-10-14

PRIOR PLING DATE: 2003-10-14

PRIOR PLING DATE: 2001-03-16

PRIOR PLING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR PLING DATE: 2001-03-16

PRIOR PLING DATE: 2000-03-16

PRIOR PLING DATE: 2000-04-4

PRIOR PLING DATE: 2000-06-14

PRIOR PLING DATE: 2000-03-22

PRIOR PLING DATE: 2000-03-22

PRIOR PLING DATE: 2000-03-22

PRIOR APPLICATION NUMBER: 09/533,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: G9 polypeptide Paralogous to G867, G993, G1930 US-10-838-616-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: 60/125,814
PRIOR PILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: 09/713,994
PRIOR FILING DATE: 2000-11-16
Sequence 4, Application US/10838616
Publication No. US20060008874A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Arabidopsis thaliana
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Query Match

29.9%; Score 53; DB 6; Length 352;

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APPLICANT: Padigaru, Muralidhara
APPLICANT: Kekuda, Ramesh
APPLICANT: Spytek, Kimberly A
APPLICANT: Leach, Martin D
APPLICANT: Shimket, Nartin D
APPLICANT: Shimket, Richard A
TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27.4%; Score 48.5; DB 7; Length 505; 40.0%; Pred. No. 32;
                                                                                                                                                                                                                                                                          US-11-07-099-6346; Application US/11087099; Sequence 6346, Application US/11087099; Publication No. US20060041961A1; GENERAL INFORMATION: GENERAL INFORMATION: GENERAL THEOFENIAR S. et al.; FILLE REFERENCE: 38-21(53450) B. EP; CURRENT APPLICANION NUMBER: US/11/087,099; CURRENT FILING DATE: 2005-03-22; NUMBER OF SEQ ID NOS: 12464; SEQ ID NO 6346
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                                                                                        ::| | ::| | ::| | ::| | | | | | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| ::| | ::| ::| ::| | ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| 
                        1 MESSLFSPSSSSYSSLFTAKPTRLLSPKPKFTFSIR 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 ESSLFSPSSSSYSSLFTAKPTRLLSPKPKFTFSIR 36
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CURRENT APPLICATION NUMBER: US/10/877,346

CURRENT FILING DATE: 2004-06-25

PRIOR PILING DATE: 2001-09-26

PRIOR FILING DATE: 2001-09-26

PRIOR FILING DATE: 2000-09-27

PRIOR PILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: 60/235,631

PRIOR APPLICATION NUMBER: 60/235,631

PRIOR APPLICATION NUMBER: 60/235,606

PRIOR PILING DATE: 2000-09-27

PRIOR PILING DATE: 2000-09-27

PRIOR PILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: 60/236,065

PRIOR APPLICATION NUMBER: 60/236,065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 2000-09-27
APPLICATION NUMBER: 60/236,135
FILING DATE: 2000-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 44, Application US/10877346
Publication No. US20060014153A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ellerman, Karen
Grosse, William M
Alsobrook II, John P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Burgess, Catherine E
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APPLICANT: MacDougall, John R
APPLICANT: Smithson, Glannda
APPLICANT: Millet, Isabelle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Neurospora crassa
US-11-087-099-6346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lepley, Denise M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/11094586
| Sequence 2, Application NO US2005027386A1
| GENERAL INFORMATION:
| APPLICANT: Allen, Stephen M. APPLICANT: Butler, Karlene H. APPLICANT: Carleon, Thomas J. APPLICANT: Stoop, Johan M. APPLICANT: PLING NATE: US/11/094,586
| CURRENT FILING DATE: 2005-03-30 |
| PRIOR PRILING DATE: 2001-07-16 |
| PRIOR APPLICATION NUMBER: US 60/218,712 |
| PRIOR PILING DATE: 2000-07-17 |
| NUMBER OF SEQ ID NOS: 32 |
| SEQ ID NO 2 |
| LENGTH: 639 |
| LENGTH: 630 |
| L
                                            13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37 SKLLSPSSSSPAVLVSSRIPLLSLRRPNLRFSVK 70
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44.8%; Pred. No. 5.2;
tive 3; Mismatches
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Sequence 1, Application US/11179624
Publication No. US20060040372A1
GENERAL INPORMATION:
APPLICANT: Sakaguchi, Nobuco
APPLICANT: Kuwahara, Kazuhiko
TITLE OF INVENTION: GANP Protein
FILE REFERENCE: 050208-0018
CURRENT PILING DATE: 2005-07-13
PRIOR APPLICATION NUMBER: PCT/JP99/04634
PRIOR PILING DATE: 2001-08-24
PRIOR FILING DATE: 2001-08-24
PRIOR FILING DATE: 2001-08-24
PRIOR FILING DATE: 2001-08-24
PRIOR FILING DATE: 2003-12-30
PRIOR FILING DATE: 2003-12-30
PRIOR FILING DATE: 1999-02-24
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.3
                                                                                                                                          1 MESSLFSPSSSSYSSLFTAKPTRLLSPKP 29
                                                                                                                                                                                                Best Local Similarity 44.8
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 29.5
Best Local Similarity 38.5
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Typha latifolia
US-11-094-586-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Mouse
US-11-179-624-1
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NAME/KEY: SIGNAL
LOCATION: (1)...(30)
US-10-517-939-52
                                                                                                                                                                                                                                                                                                                                              ORGANISM: Unknown
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Publication No. US20060024742A1

Publication No. US20060024742A1

GARBEAL INFORMATION:

APPLICANT: Martelange, Valerie

APPLICANT: De Smet, Charles

APPLICANT: De Smet, Charles

APPLICANT: BOON-FAlleur, Thierry

TITLE OF INVENTION: TUMOR ASSOCIATED NUCLEIC ACIDS AND USES THEREFOR

FILE REPERENCE: L0461.70047US01

CURRENT PELING DATE: 1096-10-30

PRIOR APPLICATION NUMBER: US/11/240,341

CURRENT PILING DATE: 1998-10-30

PRIOR APPLICATION NUMBER: US 09/103,789

PRIOR PELING DATE: 1998-10-30

PRIOR PELING DATE: 1998-04-15

NUMBER OF SEQ ID NOS: 47

SOFTWARE: PALENTING DATE: PALENTING DATE: PALOR FILING DATE: PALOR FIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
PRIOR APPLICATION NUMBER: 60/237,434
PRIOR FILING DATE: 2000-10-03
PRIOR PPLING DATE: 2000-10-05
PRIOR PILING DATE: 2000-10-05
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 127
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 48.5; DB 6; Length 1905;
Pred. No. 1.4e+02;
5; Mismatches 13; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 27.1%; Score 48; DB 7; Length 527; Best Local Similarity 42.9%; Pred. No. 39; Matches 12; Conservative 5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: SCIEL, Matter
APPLICANT: Callen, Walter
APPLICANT: Healey, Shaun
APPLICANT: Hazlewood, Geoff
APPLICANT: Wallen, David
APPLICANT: Blum, David
APPLICANT: Breeghlalian, Alireza
TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
CURRENT APPLICATION NUMBER: US/10/517,939
CURRENT APPLICATION NUMBER: US/10/517,939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 254 LDTQLTSPDSTG-EQFFTSKIVRLCVDDPKF 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MESSLFSPSSSSYSSLFTAKPTRLLSPKPKF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---RLLSPKPKF 31
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PRIOR APPLICATION NUMBER: PCT/US03/19153
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Publication No. US20060003433A1
GENERAL INFORMATION:
APPLICANT: Steer, Brian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 38.7
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-240-341-44
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                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
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12;
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                                                                                                                                                 OTHER INFORMATION: Obtained from an environmental sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MESSLFSPSSSSYS----SLFTAKPTRLLSPKFFTFSI 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13;
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                                                                                                                                                                                                                                                                                               6 FSPSSSSYSSLFTAKPTR----LLSPK-PKFTFSI
                                                                                                                                                                                                                                     Score 48; DB 6
Pred. No. 84;
4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 48;
Pred. No. 9
PRIOR FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: 60/389,299
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 380
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 52
LENGTH: 1053
TYPE: PRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3588, Application US/11072512
Publication No. US20060029945A1
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Publication No. US20050255553A1
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OTSUKI, TETSUJI
WAKAMATSU, AI
SATO, HIROYUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISHII, SHIZUKO
YAMAMOTO, JUN-ICHI
ISONO, YUUKO
HIO, YURI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 33.3%;
Matches 13; Conservative
                                                                                                                                                                                                                                     Query Match 27.1%;
Best Local Similarity 42.9%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HIO, YURI
OTSUKA, KAORU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: ISOGAI, TAKAO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens
US-11-044-051-73
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TYPE: PRT
ORGANISM: Homo sapiens
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Publication No. US20060035849A1

GENERAL INFORMATION:

APPLICANT: Spiegelman, Bruce M., et al.;

TITLE OF INVENTION: Methods and Compositions For Modulating Type I Muscle

TITLE OF INVENTION: Methods and Compositions For Modulating Type I Muscle

TITLE OF INVENTION: Mornes: US/10/514,531

CURRENT APPLICATION NUMBER: US/10/514,531

CURRENT FILING DATE: 2004-11-12

PRIOR FILING DATE: 2003-02-13

PRIOR FILING DATE: 2003-02-13

PRIOR FILING DATE: 2003-02-13

NUMBER OF SEQ ID NOS: 20

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NOS: 20
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Publication No. US20060035849A1;
GENERAL INFORMATION:
APPLICANT: Spiegelman, Bruce M., et al.;
TITLE OF INVENTION: Methods and Compositions For Modulating Type I Muscle;
TITLE OF INVENTION: Formation Using PGC-lalpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 7; Length 312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9; Indels
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APPLICANT: INTE, RYOTARD
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NADHIKO
APPLICANT: YOSHIKAWA, ICTUROU
APPLICANT: YOSHIKAWA, TSUTOUU
APPLICANT: OTSUKA, MOTOYUKI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL full length CDNA
FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT PILLING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR PILLING DATE: 2001-01-25
PRIOR PILLING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PATENTIN VEY: 2:1
SEQ ID NO 3588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26.8%; Score 47.5; D
40.7%; Pred. No. 25;
tive 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 238 SPDSEGLSSVFSSSLPSPTNSSSPSPR 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 SPSSSSYSSLFTA---KPTRLLSPKPK 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 26.8
Best Local Similarity 40.7
Matches 11; Conservative
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Best Local Similarity 35.7
Matches 15, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 SLF--SPSSSSYS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-3588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Mus musculus
US-10-514-531-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
US-10-514-531-2
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SEQUENCE LIGHT, Application US/10793626
GENERAL INFORMATION:
APPLICANT: KIMMERIN, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT FILING DATE: 1094-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PATENTIN US.: 2.1
SOFTWARE: PATENTIN US.: 2.1
LENGTH: 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 26.8%; Score 47.5; DB 6; Length 798; Best Local Similarity 35.7%; Pred. No. 72; Matches 15; Conservative 6; Mismatches 8; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 26.6%; Score 47; DB 6; Length 130; Best Local Similarity 42.4%; Pred. No. 11; Matches 14; Conservative 5; Mismatches 4; Indels
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Sequence 2465, Application US/11087099

Sequence 2465, Application US/11087099

Publication No. US20060041961A1

GENERAL INFORMATION: Genes and Uses for Plant Improvement

TITLE OF INVENTION: Genes and Uses for Plant Improvement

FILE REFERENCE: 38-21 (53450) B EP

CURRENT PPLICATION NUMBER: US/11/087,099

CURRENT FILING DATE: 2005-03-22

NUMBER OF SEQ ID NOS: 12464

SEQ ID NO 2465

LENGTH: 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  532 SLFNVSPSCSSFNSPCRDSVSPPKSLFSQRPQRMRSRSRSFS 573
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US-11-087-099-2465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 SSLFSPSSSSYSSLFTAKPTRLLSPKPKFTFSI 35
FILE REFERENCE: DFN-041US
CURRENT APPLICATION NUMBER: US/10/514,531
CURRENT FILING DATE: 2004-11-12
FRIOR APPLICATION NUMBER: PCT/US03/04792
PRIOR FILING DATE: 2003-02-13
PRIOR FILING DATE: 2003-02-13
PRIOR FILING DATE: 2002-02-13
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PastSEQ for Windows Version 4.0
SOFTWARE: 798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
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APPLICANT: KYOWA HAKKO KOGYO CO., LTD.
TITLE OF INVENTION: Process for producing dipeptides or dipeptide derivatives
FILE REFERENCE: 4093-13
CURRENT APPLICATION NUMBER: US/11/165,226
CURRENT FILING DATE: 2005-02-4
PRIOR PILING DATE: 2004-06-25
PRIOR FILING DATE: 2004-06-25
RIOR FILING DATE: 2004-06-25
SOFTWARE: PatentIN Ver. 2.1
SEQ ID NO 124
LENGTH: 688
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                                               Gaps
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                                               12;
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Score 47; DB 7; Length 161;
Pred. No. 14;
6; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 11997, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REPERENCE: 38-21 (53450) B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT PILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 11997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 47; DB 7; Length 688;
Pred. No. 71;
3; Mismatches 11; Indels
                                                                                                             1 MESSLFSPSSSSYSSLFTAKPTRLLS------PKP
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; ORGANISM: Pseudomonas syringae pv. syringae B728a
US-11-087-099-11997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MESSLFSPSSSSYSSLFTAKPTRLL 25
                                                                                                                                                                                                              US-11-165-226-124; Sequence 124, Application US/11165226; Publication No. US20050287627A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: BRT
; ORGANISM: Eschierichia coli W3110
US-11-165-226-124
Query Match 26.6%;
Best Local Similarity 31.7%;
Matches 13; Conservative
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1 Similarity 44.0%;
11; Conservative
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Best Local Similarity
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US-11-087-099-11997
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Search completed: March 7, 2006, 22:06:39 Job time : 16.6 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

March Run on:

7, 2006, 21:53:39 ; Search time 28.8 Seconds (without alignments) 120.271 Million cell updates/sec

Title: Perfect score:

US-10-751-235-11 177 1 MESSLFSPSSSSYSSLFTAKPTRLLSPKPKFTFSIR 36 Sequence:

**BLOSUM62** Scoring table:

283416 seqs, 96216763 residues Gapop 10.0 , Gapext 0.5 Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 80:\*
!: pir::\*
!: pir2:\*
!: pir3:\*
!: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		di			SUMMARIES	
Result No.	Score	Query	Length	DB	, QI	Description
-	177	100.0	566	7	T46159	cytochrome P450-1
8	65.5	m	430	7	T50296	conserved hypothet
e	9	33.	355	Н	JQ2256	phosphoribosylform
4	9	33.9	389	7	T47640	phosphoribosylform
S	•	щ	319	~	A85437	hypothetical prote
9	58.5		351		.T19059	
7	26		474		T45818	hypothetical prote
80	26	31.6	883		S04722	puff 74B protein.
6		31.1	406		T48103	mRNA binding prote
10		30.8	612		T38714	hypothetical prote
11	54.5	30.8	1621	7	T30200	protein-tyrosine
12	54	ö	132	~	A75491	hypothetical prote
13	54	ö	205	~	T47591	aintegumaenta-like
14	54	ö	403	~	T45712	NAD-dependent mala
15	54	30.5	403	7	T51862	malate dehydrogena
16	53.5	ö	1564		855517	probable transport
17	53	29.9	352		TS1330	DNA binding protei
18	53	29.9	915		A55144	autotaxin precurso
19	52.5	29.7	402		A84766	hypothetical prote
	52.5	29.7	411		T51818	ATP phosphoribosy
21	25	29.4	159		D71033	hypothetical prote
22	52	29.4	246		T30490	
23	52	29.4	320		T31547	
24	52	29.4	2606		T03159	_
25	51.5	29.1	272		H71124	hypothetical prote
26	51	28.8	211		C84751	
27	51	8	299		T52452	ATP-dependent Clp
	51	28.8	354		.T49806	hypothetical prote
29	51	28.8	446	~	T45525	

UDP-N-acetylmuramo	protein kinase hom	protein C23F12.1 [	hypothetical prote	polyphosphate kina	polyphosphate kina	extensin homolog T	probable G-protein	hypothetical prote	hypothetical prote						
AH3323	S52494	B89608	T15571	T01998	T00679	S54461	T18883	E84849	T05758	AE0345	AC0819	T14195	E86443	T19823	F72746
N	~	N	N	~	~	ď	N	N	~	~	~	7	~	~	7
499	620	2305	2305	361	632	960	1390	291	562	687	688	707	848	1695	113
28.8	28.8	28.8	28.8	28.5	28.5	28.5	28.5	28.2	28.2	28.2	28.2	28.2	28.2	28.2	28.0
51	51	51	21	50.5	50.5	50.5	50.5	20	20	20	20	20	20	20	49.5

# ALIGNMENTS

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R.) Wakatura, G.; Fartmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.; N. submitted to the Protein Sequence Database, December 1999
A; Reference number: Z23025
              N;Alternate names: protein T4D2.60
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C;Accession: T46159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:Q9SCP8; UNIPARC:UPI00009D7F9; EMBL:AL132958
A;Experimental source: cultivar Columbia; BAC clone T4D2
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Keywords: heme; iron; metalloprotein
F;371-536/Domain: cytochrome P450 homology <P45>
F;514/Binding site: heme iron (Cys) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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A;Introns: 183/2; 292/3; 358/3; 392/3; 439/3; 475/3; 503/2; 557/3
A;Note: T4D2.60
C;Superfamily: pea cytochrome P450 CXP97; cytochrome P450 homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 177; DB 2; Length 566; Best Local Similarity 100.0%; Pred. No. 1e-15; Matches 36; Conservative 0; Mismatches 0; Indels
cytochrome P450-like protein - Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                             A, Molecule type: DNA
A, Residues: 1-566 < NYA>
                                                                                                                                                                                                                                                                                                                           Status: preliminary
                                                                                                                                                                                                                                                                                          Accession: T46159
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### RESULT 2

- fission yeast (Schizosaccharomyce: conserved hypothetical SH3 domain protein [imported] - fission yeast (Schizc conserved hypothetical SH3 domain protein [imported] - fission yeast (Schizc C:Species: Schizosaccharcmyces pombe
C;Date: 09-Jun-2000 #sequence\_revision 09-Jun-2000 #text\_change 09-Jul-2004
C;Accession: T50296
R;McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Brown, S.; Harris, D. A;Reference number: Z25040
A;Reference number: Z25040
A;Accession: T50296

Status: preliminary; translated from GB/EMBL/DDBJ; Molecule type: DNA

A;Gross-references: UNIPROT:09URW6; UNIPARC:UPI000006AE4A; EMBL:AL133359; PIDN:CAB62422.1 A;Experimental source: strain 972h(-) Residues: 1-430 <MCD>

C;Genetics

Gene: SPDB:SPAPJ696.02 A, Map position: 1 2

Gaps

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A,Note: T15C9.10
C,Superfamily: phosphoribosylformylglycinamidine cyclo-ligase, phosphoribosylformylglycir
                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: UNIPARC: UPI0000048D08; GB:NC_001268; NID:97270649; PIDN: CAB80366.1; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-351 <WIL>
A;Gross-references: UNIPROT:Q17793; UNIPARC:UPI000007AE93; EMBL:Z49908; PIDN:CAA90104.1;
A;Experimental source: clone C0783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPARC:UPI000007AE93; EMBL:Z49070; PIDN:CAA88872.1; GSPDB:GN00020; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein T09F3.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T19059; T24756
R;Matthews, P. BMBL Data Library, June 1995
A;Reference number: Z19066
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 319;
                                                                           Length 389;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 33.6%; Score 59.5; DB 2; Best Local Similarity 43.8%; Pred. No. 2.3; Matches 14; Conservative 7; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5;
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A;Molecule type: DNA
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33.1%; Score 58.5; DE
Best Local Similarity 46.2%; Pred. No. 3.5;
Matches 18; Conservative 5; Mismatches
                                                                           Score 60; DB 2
Pred. No. 2.5;
6; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Introns: 20/3; 122/3; 188/3; 241/2; 274/2
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                                                                           7 Match 33.9%;
Local Similarity 42.1%;
nes 16; Conservative
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A; Residues: 1-351 <WI2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: A85437
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-319 <STO>
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Dyesthoribosylformylglycinamidine cyclo-ligase (EC 6.3.3.1) precursor - Arabidopsis thal

NyAlternate names: 5'-phosphoribosyl-5-aminoimidazole synthetase; protein F28P10.10

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 30-Sep-1993 #sequence_revision 28-Oct-1994 #text_change 15-Oct-1999

C;Accession: J02256; T06719

Plant Physiol. 102, 387-399, 1993

A;Fitle: Isolating the Arabidopsis thaliana genes for de novo purine synthesis by suppre

A;Reference number: J02256; MUD: 94151435; PMID: 8108507

A;Reference number: J02256; MUD: 94151435; PMID: 8108507

A;Residues: 1-355 <SEN>

A;Residues: 1-355 <SEN>

A;Residues: 1-355 <SEN>

B;Ouetier, F; Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artigu

submitted to the Protein Sequence Database, April 1999

A;Reference number: Z15793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A Map position: 3
A;Introns: 102/1
A;Introns: 102/1
S;Superfamily: phosphoribosylformylglycinamidine cyclo-ligase; phosphoribosylformylglyci
C;Keywords: cyclo-ligase; purine nucleotide biosynthesis
B;1-58/Domain: signal sequence #status predicted <SIG>
F;59-355/Product: phosphoribosylformylglycinamidine cyclo-ligase #status predicted <MAT>
F;69-355/Domain: phosphoribosylformylglycinamidine cyclo-ligase homology <PFCL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Molecule type: DNA
A,Residues: 1-125 <QUES.
A,Residues: 1-125 <QUES.
A,Residues: 1-125 <QUES.
A,Experimental source: UNIPARC:UPI000016DB1E; EMBL:AL049655; ATSP:F28P10.10; GSPDB:GN00061
A,Experimental source: cultivar Columbia; BAC clone F28P10
C,Comment: This enzyme is involved in the fifth step of the purine biosynthetic pathway, C,Genetics:
A,Gene: ATSP:F28P10.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 4
T47640
phosphoribosylformylglycinamidine cyclo-ligase precursor - Arabidopsis thaliana
N;Alternate names: protein T15C9.10
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T47640
R;Mewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.P.X.
submitted to the Protein Sequence Database, April 2000
A;Accession: T47640
A;Status: preliminary
A;Accession: T47640
A;Status: preliminary
A;Accession: T47640
A;Essiques: 1.389 -AEM>
A;Cross-references: UNIPROT:QO5728; UNIPARC:UPI00000017F6; EMBL:AL132970
A;Experimental source: cultivar Columbia; BAC clone T15C9
C;Genetics:
A;Map position: 3
A;Introns: 102/1; 133/3; 167/3; 187/3; 245/2; 279/3; 332/3
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7
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9
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                                                        Length 430;
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                                                                                                                Indels
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                                                                                                                9
                                               ch 37.0%; Score 65.5; DB 2; 1 Similarity 55.2%; Pred. No. 0.51; 16; Conservative 2; Mismatches 6;
                                                                                                                                                                                                 343 SSQFSSRSSEYS----KPSRPTAPKPKF 366
                                                                                                                                                                     3 SSLFSPSSSSYSSLFTAKPTRLLSPKPKF 31
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hes 16; Conservative
                                                                                       Best Local Similarity
        A; Introns: 13/1; 26/3
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                                                           Query Match
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C;Accession: T48103
R;Obermaier, B.; Ottenwaelder, B.; Duchemin, D.; Zeitler, K.; Mewes, H.W.; Rudd, S.; Lemc Bubmitted to the Protein Sequence Database, April 2000
A;Reference number: Z24484
A;Accession: T48103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: T30200

C;Accession: T30200

R;Iwahara, T.; Fujimoto, J.; Wen, D.; Cupples, R.; Bucay, N.; Arakawa, T.; Mori, S.; Rat;
Oncogene 14, 439-449, 1997

A;Title: Molecular characterization of ALK, a receptor tyrosine kinase expressed specific
A;Reference number: Z20774; MUID:97178863; PMID:9053841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:Q10187; UNIPARC:UP1000013A18B; EMBL:Z69369; PIDN:CAA93311.1; A;Experimental source: strain 972h-; cosmid c3F10
                                                                                                                       nRNA binding protein CSP41 homolog T20010.240 [similarity] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) 2;Species: Arabidopsis thaliana (mouse-ear cress) 2;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
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C;Superfamily: Schizosaccharomyces pombe hypothetical protein SPAC3F10.13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:Q9LXA9; UNIPARC:UPI00009DE02; EMBL:AL163816
A;Experimental source: cultivar Columbia; BAC clone T20010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R.Murphy, L.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V. submitted to the EMBL Data Library, Pebruary 1996
A;Reference number: Z21807
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 SSLFSPSSSSYSSLF-----TAKPTRLLSPKPKFTFSIR 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 31.1%; Score 55; DB 2;
Best Local Similarity 58.1%; Pred. No. 12;
Matches 18; Conservative 4; Mismatches .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: T38714
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
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Pred. No. 22;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41 SSLSSSSSSSLLTFSLRTSRRLSPQ-KFT 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 SSLFSPSSSSYSSL-FTAKPTRLLSPKPKFT 32
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N;Alternate names: anaplastic lymphoma kinase
C;Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Map position: 3
A;Introns: 132/3; 173/2; 207/3; 254/1; 346/3
A;Note: T20010.240
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Best Local Similarity 32.6%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Gene: SPDB:SPAC3F10.13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Residues: 1-406 <OBE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: T30200.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Accession: T38714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nypothetical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C:Genetics:
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                                                                                                                                                                                                                                                                                            hypothetical protein F2809.250 - Arabidopais thaliana C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C; Accession: T45818
R; Benes, V.; Rechmann, S.; Borkova, D.; Ansorge, W.; Mewes, H.W.; Lemcke, K.; Mayer, K.F submitted to the Protein Sequence Database, January 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: S04722; B34692
R;Janknecht, R.; Taube, W.; Luedecke, H.J.; Pongs, O.
RvJanknecht, R.; Taube, W.; Luedecke, H.J.; Pongs, O.
RvJanknecht: Acids Res. 17, 4455-4464, 1989
A;Title: Characterization of a putative transcription factor gene expressed in the 20-OH
A;Reference number: S04722; MUID:89315191; PMID:2501755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: 1-883 «JAN»
A; Residues: 1-883 «JAN»
A; Cross-references: UNIPROT: P11536; UNIPARC: UP10000129AFF; EMBL: X15087; NID: 97513; PIDN: A; Cross-references: Universe: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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A;Cross-references: UNIPARC:UP100001247C8; GB:M37083; NID:g157309; PID:g157310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     puff 74B protein - fruit fly (Drosophila melanogaster)
NiAlternate names: eddysone-induced protein E74B; ets-related protein E74B
C:Species: Drosophila melanogaster
C:Species: 28-Peb-1990 #sequence_revision 28-Peb-1990 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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A;Experimental source: cultivar Columbia; BAC clone F2809
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A;Map position: 3 74FF
Cs/Keywords: alternative splicing; DNA binding; transcription regulation
F;789-869/Domain: ets DNA-binding domain homology <FTS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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C;Superfamily: Arabidopsis thaliana hypothetical protein F2809.250
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Pred. No. 21;
2; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 56; DB 2; Length 474;
Pred. No. 10;
5; Mismatches 8; Indels
                                                  73 SSMPAASSPSAAATYSTVTTAALVVPTTLQSPKREFVCS 111
SSLFSPSSSS----YSSLFTAK---PTRLLSPKPKFTFS 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPSSSSSPATTLFRSRSSRLLLSKAQSTISI 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPSSSSYS----SLFTAKPTRLLSPKPKFTFSI 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39 SSLSLSSSSSSSSLSSATPTVASP 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 48.5%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31.6%;
ilarity 60.0%;
Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Accession: T45818
A, Status: preliminary
A, Molecule type: DNA
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4; Mismatches

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7 SPSSSSYSSLFTAKPTRLLSPKPK 30
    12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary A; Molecule type: DNA
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    Matches
                                                                                                                                                                                                                                                                                     RESULT 14
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NiAlternate names: protein T12E18.10
C;Specias: Arabidopsis thaliana (mouse-ear cress)
C;Specias: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T47591
R;Blocecker, H., i Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quetier, F.; Salanoubat M.Mewes, submitted to the Protein Sequence Database, March 2000
A;Reference number: Z24469
A;Reternce number: Z24469
A;Reterns preliminary
A;Molecule type: DNA
A;Reternces: UNPROT:Q9M2V4; UNIPARC:UP100000AAF3C; EMBL:AL132971
A;Experimental source: cultivar Columbia; BAC clone T12E18
C;Genetics:
A;Map position: 3
A;Introns: 71/2; 99/1; 128/3; 170/2
A;Note: T12E18.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein - Deinococcus radiodurans (strain R1)
c;Species: Deinococcus radiodurans
c;Species: Dainococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: A75491
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.G.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A; Residues: 1-1621 <1WA>
A; Residues: 1-1621 <1WA>
A; Cross-references: UNIPROT: P97793; UNIPARC: UPI000029516; EMBL: D83002; NID: 91864006; P1
A; Experimental source: brain and testis
C; Genetics:
A; Genetics:
A
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A;Residues: 1-132 <WHI>
A;Cross-references: UNIPROT:Q9RWL1; UNIPARC:UPI0000C17C8; GB:AE001923; GB:AE000513; NID
A;Experimental source: strain R1
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C;Superfamily: Deinococcus radiodurans hypothetical protein DR0655
                                                                                                                                                                                                                                                                                                                                                                Length 1621;
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Pred. No. 7.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                           7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10; Indels
                                                                                                                                                                                                                                                                                                                                                            30.8%; Score 54.5; DB 2;
44.4%; Pred. No. 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 30.5%; Score 54; DB 2;
1 Similarity 48.4%; Pred. No. 4.6;
15; Conservative 4; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 SALAQPASSSVGYSSLVSAVPQRVTLPLQLF 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 SSLFSPSSSS--YSSLFTAKPTRLLSPKPKF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 SSLFSPSSSSYSSLFTAKPTRLLSPKP 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30.5%;
                                                                                                                                                                                                                                                                                                                                                                    Query Match 30.8%;
Best Local Similarity 44.4%;
Matches 12; Conservative
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Best Local Similarity
Matches 15, Conserva
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C,Genetics:
A,Gene: DR0655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
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C,Accession: T45712
C,Accession: T45712
R;Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.; Sau
submitted to the Protein Sequence Database, November 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Berkemeyer, M.; Scheibe, R.; Ocheretina, O.
J. Biochem. 273, 27927-27933, 1998
A;Title: A novel, non-redox-regulated NAD-dependent malate dehydrogenase from chloroplast
A;Reference number: 225488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;Cross-references: UNIPROT:081844; UNIPARC:UPI0000A9B2A; EMBL:Y13987; PIDN:CAA74320.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              malate dehydrogenase (BC 1.1.1.37), chloroplast [validated] - Arabidopsis thaliana C,Species: Arabidopsis thaliana (mouse-ear cress)
C,Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ä
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                                                                                                                                              NAD-dependent malate dehydrogenase, chloroplast - Arabidopsis thaliana N;Alternate names: protein F1P2.70 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gross-references: UNIPROT:09SN86; UNIPARC:UPI00000AC228; EMBL:AL132955 A;Experimental source: cultivar Columbia; BAC clone FIP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 30.5%; Score 54; DB 2; Length 403; Best Local Similarity 47.1%; Pred. No. 16; Matches 16; Conservative 3; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 403;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 54; DB 2;
Pred. No. 16;
3; Mismatches 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;Status: preliminary; translated from GB/EMBL/DDBJ;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SELFSTVSSSYSKASSIPHSRLQSVKFNSVPSFT
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C;Superfamily: L-lactate dehydrogenase
C;Keywords: chloroplast; NAD; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: March 7, 2006, 21:59:04
13 SPSSSVSSSTTTSSPIQSEAPRPK 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Genome: nuclear
A,Note: FIP2.70
C.Superfamily: L-lactate dehydrogenase
C,Keywords: chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 47.1%;
Matches 16; Conservative
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Job time : 30.8 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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OM protein - protein search, using sw model

March Run on:

7, 2006, 21:43:16 ; Search time 178.2 Seconds (without alignments) 142.531 Million cell updates/sec

US-10-751-235-11

Perfect score:

1 MESSLFSPSSSSYSSLFTAKPTRLLSPKPKFTPSIR 36 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2166443 seqs, 705528306 residues

Searched:

Total number of hits satisfying chosen parameters:

2166443

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

UniProt\_05.80:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

																_	_	_			_		_								_
tion	arabidopsis	arabidopsis	arabidopsis	schizosacch	drosophila	drosophila	aspergillus	arabidopsis	arabidopsis	neurospora	drosophila	mus musculu	caenorhabdi	chamaecypar	dictyosteli	trypanosoma	cryptococcu	cryptococcu	cryptospori	plasmodium	arabidopsis	dictyosteli	dictyosteli	parachlamyd	caenorhabdi	neurospora	mus musculu	arabidopsis	mus musculu	arabidopsis	arabidopsis
Description	Q6tbx7	Q8 rwv4	Q9scp8	O9urw6	Q8mdd8		Q5b1u5		081du4		Q9vyn1	04h4d7	Q17793	Q75wn1	Q86h13	Q57up3	055p26	Q5ked0	069316	Q4xca2	09c589	Q86a82	Q555x3	Q6maz9	Q620q0	Q8x0n1	Q9d347	Q81ed3			Q8w418
			•																								•				
QI	Q6TBX7 ARATH	Q8RWV4 ARATH	Q9SCP8 ARATH	Q9URW6 SCHPO	Q8MQQ8_DROME	Q9VLS7 DROME	Q5B1US EMENI	PURS ARATH	RCCR_ARATH	Q7S9IO NEUCR	Q9VYN1_DROME	Q4H4D7 MOUSE	Q17793 CAEEL	Q75WN1 CHAOB	Q86H13_DICDI	Q57UP3_9TRYP	Q55P26 CRYNE	Q5KED0 CRYNE	Q693I6_CRYHO	Q4XCA2 PLACH	Q9C589 ARATH	Q86A82_DICDI	QSSSX3 DICDI	Q6MAZ9 PARUW	Q620Q0 CAEBR	Q8X0N1 NEUCR	Q9D347 MOUSE	Q8LED3 ARATH	Q5F245 MOUSE	Q9M2K7_ARATH	Q8W4L8_ARATH
·B	7	~	~	~	~	~	~	-	-	~	~	~	7	0	~	~	~	~	~	7	~	~	~	7	~	~	7	~	~	~	~
Length DB	539	552	266	430	1332	2016	1383	389	319	624	1545	1733	355	605	771	2408	512	513	126	144	302	1449	1464	497	577	353	357	434	459	474	476
& Query Match	100.0	100.0	100.0	37.0	35.3	35.3	34.7	33.9	33.6	33.3	33.3	33.3	33.1	32.8	32.8	32.8	32.5	32.5	32.2	32.2	32.2	32.2	32.2	31.9	31.9	31.6	31.6	31.6	31.6	31.6	31.6
Score	177	177	177	65.5	62.5	62.5	61.5	9	59.5	29	59	29	58.5	28	28	28	57.5	57.5	57	57	57	57	57	56.5	56.5	99	26	26	99	26	26
Result No.	1	7	٣	4	S	9	7	œ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31

	Dileik Arosophile				Q8la28 arabidopsis	Q9lya9 arabidopsis	Q6j735 sorghum bic	Q4rm98 tetraodon n	Q6zfu9 oryza sativ			Q86z12 podospora a		Q8ciq7 mus musculu
TOTION LANGS	SOCIET STATE	PART OF THE PART O	QSSSDZ_DICDI	Q869R4_DICDI	Q8LA28_ARATH	Q9LYA9_ARATH	Q6J735_SORBI	Q4RM98_TETNG	Q6ZFU9 ORYSA	Q6Z8R9 ORYSA	UCP6_SCHPO	Q86ZL2 PODAN	ALK MOUSE	DOCK3_MOUSE
707	100	200	1001	1806 2	143 2	406 2	818 2	836 2	138 2	416 2	612 1	696 2	1621 1	2027 1
31.6	31.6	0.10	31.6	31.6	31.1	31.1	31.1	31.1	30.8	30.8	30.8	30.8	30.8	30.8
9 1		ף ע ה	9	26	22	22	22	55	54.5	54.5	54.5	54.5	54.5	54.5
,,	4 6	2 .	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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Gaps
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Tian L., Musetti V., Kim J., Magallanes-Lundback M., DellaPenna D.;
"The Arabidopsis LUT1 locus encodes a member of the cytochrome p450
"amily that is required for caroteenoid epsilon-ring hydroxylation
                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana (Mouse-ear cress).
Wataryota, Vitidiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; eudicotyledons; core eudicotyledons; Cosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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PRINTS; PR00385; P450.
PROSITE; PS00086; CYTCCHROME_P450; UNKNOWN 1.
Heme; Iron; Metal-binding; Monooxygenase; Öxidoreductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 101:402-407(2004).
-1- SIMILARITY: Belongs to the cytochrome P450 family.
EMBL. AY424605; AAR8120.1; "RNA.
GO; GO:0046872; F:metal ion binding; IEA.
GO; GO:0004497; F:metal ion binding; IEA.
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR001128; Cytochrome_P450.
Pfam; PF00067; P450; 1.
                                                                                                                                                    05-JTL-2004 (TrEMBLrel. 27, Created)
05-JTL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Chloroplast carotenoid epsilon-ring hydroxylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 177; DB 2;
100.0%; Pred. No. 9.8e-15;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MESSLFSPSSSSYSSLFTAKPTRLLSPKPKFTFSIR 36
                                                                            539 AA.
                                                                            PRT;
                                                                   QGTBX7_ARATH PRELIMINARY;
QGTBX7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 100.
Les 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transmembrane
                                                                                                                                                                                                                                                                                                                         Name=LUT1;
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MESSLFSPSSSSYSSLFTAKPTRLLSPKPKFTFSIR 36 ARATH 셤

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QBRWV4 ARATH PRELIMINARY; PRT; 552 AA. QBRWV4; 01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) RESULT 2 Q8RWV4 AR ID Q8RW AC Q8RW DT 01-J DT 01-J DT 01-M

Putative cytochrome P450 (Fragment).

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Indels

2; Length 566;

us-10-751-235-11.rup

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MEDINESITHMENT PURPORELIES STORY OF STEAMER S. STEWART A. MEDINESITHMENT PURPORELIES STORY OF STATEMENT S. STEWART A. STEWART S. HORDRAD S. HORDRAD S. HOLTONG S. HOLTONG S. HOLTONG S. HOLTONG S. HOLTONG S. MCDOMAIG S. MCLOMAN S. MCCONDIA S. MCCOMDIA S. M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
                                                                                                                                                           PROSITE; PS00086; CYTOCHROME P450; UNKNOWN 1.
Heme; Iron; Metal-binding; Monooxygenase; Oxidoreductase;
                                                                                                                                                                                                                                                    566 AA; 63596 MW; B884E8996B1A4C7D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Pungi, Ascomycota, Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                        1 MESSLFSPSSSSYSSLFTAKPTRLLSPKPKFTFSIR 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MESSLFSPSSSSYSSLFTAKPTRLLSPKPKFTFSIR 36
                                                                                                                                                                                                                                                                                                         100.0%; Score 177; DB 2;
100.0%; Pred. No. 1e-14;
:ive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           430 AA
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EMBL; AL133359; CAB62422.1; -; Genomic_DNA.
PIR; T50296; T50296.
  GO; GO:0006118; P:electron transport; IEA
                       InterPro; IPR001128; Cytochrome_P450
InterPro; IPR002401; EP4501.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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GeneDB Spombe; SPAPJ696.02;
InterPro; IPR007461; DUF500.
InterPro; IPR001452; SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.(
Matches 36; ConBervative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9URW6 SCHPO PRELIMINARY;
Q9URW6;
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                                                                         PERM; PF00067; P450; 1.
PRINTS; PR00463; EP450I.
PRINTS; PR00385; P450.
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ORFNames=SPAPJ696.02;
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Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,

A Deng J.W., Goldmanth A.D., Lee J.M., Omodera C.S., Quacch H.L.,

Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,

Carninci P., Chen H., Kh. Hayashizaki Y., Ishidda J., Jones T.,

Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,

Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,

Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,

Sakurai T., Satou M., Saki M., Shinn P., Southwick A., Shinozaki K.)

Bavis R.W., Ecker J.R., Theologis A.;

Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

LISIMILARITY: Belongs to the cytochrome P450 family.

EMBL; AY091083; AAM13903.1; -; mRNA.

RO; GO:0046872; F:metal ion binding; IEA.

GO; GO:0046872; F:metal ion binding; IEA.

GO; GO:006118; P:electron transport; IEA.

RO; GO:006118; P:electron transport; IEA.

InterPro; IPR002401; EP4501.

R InterPro; IPR00385; P450.

R RINTS; PR00463; P4850.

R PRINTS; PR00463; P4850.

R PRINTS; PR00463; P4850.

R PRINTS; PR0066; CYTOCHROME P450; UNKNOWN 1.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2004 (TrEMBLrel. 26, Last annotation update)
Cytochrom P450-like protein.
Name=T4D2.60;
Arabidopsis thallana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicotyledons; cosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
Name-At3g53130;
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EU Arabidopsis sequencing project;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
1-1. SINILARIT'S Belongs to the cytochrome P450 family.
EMBL: AL132958; CAB64216.1; -; Genomic_DNA.
PIR; T46159; T46159.
PIR; T46159; T4675;
GO: GO:0046872; F:metal ion binding; IEA.
GO: GO:004497; F:metal ion binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  552 AA; 62073 MW; C23CF8498B5B8440 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MESSLFSPSSSSYSSLFTAKPTRLLSPKPKFTFSIR 36
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Q9SCP8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 36; Conservative
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                                                                                                                  rosids; eurosids
NCBI_TaxID=3702;
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Gaps
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2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35.3%; Score 62.5; DB 2; Length 1332; 47.4%; Pred. No. 41; cive 4; Mismatches 11; Indels 5
                                                                        Length 430;
                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygo
Neptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Bphydroidea, Drosophilidae, Drosophila.
                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1332 AA; 144944 MW; B3F3F5931D907008 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AX128444; AAM75071; -; mRNA.
Ensembl; CG8552; Drosophila melanogaster.
FlyBase; FBGN0031990; CG8552.
                             PROSITE; PS50002; SH3; 1.
Complete protecome; SH3 domain.
SEQUENCE - 430 AA; 46373 MW; AC300C08C29D946F CRC64;
                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSLFSPSQVDSTSSLFAPPTSANTTILTPAPDTTSTL 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
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                                                                                             9
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                                                                       Score 65.5; Di
Pred. No. 4.4;
2; Mismatches
                                                                                                                            343 SSQPSSRSSEYS----KPSRPTAPKPKF 366
                                                                                                                3 SSLFSPSSSSYSSLFTAKPTRLLSPKPKF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0046872; P:metal ion binding; IEA
                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=CG8552; ORFNames=CG8552;
                                                                        37.0%;
55.2%;
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01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2004 (TrEMBLrel. 26,
CG8552-PA.
; PR00452; SH3DOMAIN.; PD000066; SH3; 1.
SM00326; SH3; 1.
                                                                                                                                                                                 QBMQQ8_DROME PRELIMINARY;
Q8MQQ8;
                                                                  Ouery Match
Best Local Similarity 55.2°
Matches 16; Conservative
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InterPro; IPR004170; WWE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 47.4 ies 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF02862; DDHD; 1.
Pfam; PF02825; WWE; 1.
                                                                                                                                                                                                                                            LD21041p (Fragment).
ORFNames=CG8552;
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A Arachohi H.M., Barna N., Bastien V., Bloom T., Boguslavkiy L.,
A Boukhgalter B., Butler J., Calvo S.B., Camazta J., Chang J.,
Choepel Y., Collymore A., Cook P., Corum B., DeArellano K.,
Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
B Erickson J., Faros S., Farreira P., FitzGerald M., Cage D., Galagan J.,
R Erickson J., Faros S., Farmain L., Grand-Pierre N., Hafez N.,
Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
Johnson R., Jones C., Kamal M., Kamat R., Karatas A.,
Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
Ma L.-J., Mabbitt R., MacLean C., Macdonald P., Major J., Manning J.,
Mathews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,
Milova T., Mlenga V., Murphy T., Maylor J., Nguyen C., Nicol R.,
Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D.,
O'liver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
Rachupka A., Ramassamy U., Raymond C., Retta R., Rise C., Rogov P.,
R Roman J., Schauer S., Schupback R., Sesman S., Severy P., Smirnov S.,
Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                 Derkeley Drosophila Genome Project, Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R., Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E. Yu C., Rubin G., "

"Drosophila melanogaster release 4 sequence."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                       Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2
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Eurotiales; Trichocomaceae; Emericella.
                                                                                                                                                                                                                                                                                                                                                                                          Q9VCB1:CG13609; NbExp=1; IntAct=EBI-190906, EBI-105274; EMBL; AE003620; AAF52607.1; -; Genomic_DNA.
IntAct; Q9VLS7; EDSOphila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 62.5; DB 2; Length 2
Pred. No. 67;
4; Mismatches 11; Indels
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                                                                                                                                                                                                                                                                                                                                            Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases
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                                                                Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FlyBase; FBGn0031990; GG8552.
GO, GO:0046872; F:metal ion binding; IEA.
InterPro; IPR004177; DDHD.
InterPro; IPR004170; WWE.
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10-MAY-2005 (TrEMBLrel. 30, Last
10-MAY-2005 (TrEMBLrel. 30, Last
Hypothetical protein.
ORFNames-ANS-485.2;
Aspergillus nidulans FGSC A4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47.48;
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Best Local Similarity 47.45
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QSB1US;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF02862; DDHD; 1.
Pfam; PF02825; WWE; 1.
PROSITE; PS50918; WWE; 1.
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                                             systematic review
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REC STRAIN-CV Columbas,

KREDLINE-21016720; PubMed=11130713; DOI=10.1038/35048706;

RA Salanoubat M., Lemcke K., Rieger M., Ansorge W., Unseld M.,

RA Belseny M., Lemcker H., Perez-Alonso M., Obermaler B.,

RA Delseny W., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,

RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier P.,

RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier P.,

RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier P.,

RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier P.,

RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Gres V.,

RA Wincker P., Cattolico L., Weissenbach J., Sandon R.,

RA Wincker P., Collado C., Perez-Perez A., Toppo S., Simionati B.,

Rocke R., Laudie M., Barger-Llauro C., Purnelle B., Mawuy D.,

RA Monfort A., Argiriou A., Flores M., Liguori R., Vitale D.,

RA Monfort A., Alcarez J.-P., Cottet A., Casacuberta E.,

RA Monfort A., Raisiou A., Flores M., Liguori R., Vitale D.,

RA Manhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,

RA Rooney T., Rizzo M., Walte A., Utterback T., Puili C.Y., Shea T.P.,

RA Rooney T., Rizzo M., Walte A., Gill J.E., Feldblyum T.V.,

RA Pai G., Milltscher J., Sellers P., Gill J.E., Feldblyum T.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            synthesis
Talamas J., Tesfaye S., Theodore J., Topham K., Travers M., Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B., Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M., Lander E.;
                                                                                                                                                                                         "Genome Sequence of Aspergillus nidulans.";
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AACD100094; EAA62645.1; -; Genomic_DNA.
InterPro; IPR011993; PH_type.
InterPro; IPR000156; Ran_BPI.
Fam; PF00638; Ran_BPI; 1.
PROSITE; PS50196; RANBDJ; 1.
PROSITE; PS50196; RANBDJ; 1.
PROSITE; PS50196; RANBDJ; 1.
PROSITE; PS50196; RANBDJ; 1.
SAGUENCE 1383 AA; 141244 MW; D7F854C0423511E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         synthase).
Name=PURS; OrderedLocusNames=At3g55010; ORFNames=T15C9.10, F28P10.10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     005728; Q9N2W5; Q9SV49; 01-NVV-1995 (Rel. 32, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 13-SEP-2005 (Rel. 48, Last annotation update) Phosphoribosylformylglycinamidine cyclo-ligase, chloroplast precurse (EC 6.3.3.1) (AIRS) (Phosphoribosyl-aminoimidazole synthetase) (AIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Senecoff J.F., Meagher R.B.; Insolating the Arabidopsis thaliana genes for de novo purine synthem by suppression of Bacharichia coli mutants. I. 5'-Phosphoribosyl-5-aminoimidazole synthetase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).
Mukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons, rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 1383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAINECY. Columbia; TISSUB-Leaf, and Stem;
MEDLINE-94151435; PubMed-8108507; DOI=10.1104/pp.102.2.387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 SLFSPSSSS------YSSLFTAKPTRLLSPKPK 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34.7%; Score 61.5; D
37.5%; Pred. No. 58;
iive 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plant Physiol. 102:387-399(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 37.5
hes 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=3702;
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RCCR ARATH

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                                                                                                                                                                                                                      STRAIN=CV. Columbia; Carlo Coll. 126/Science. 1088305; MEDLINE=22954869; PubMed=14593172; DOI=10.1126/Science.1088305; Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J., Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J., Chen K., Lim S.X., Lam B., Sakano H., Wu T., Yu G., Miranda M., Quach H.L., Tripp M., Chan G.H., M. Tang C.L., Lee J.M., Athama K., Ansari Y., A Chan M.M., Tang C.C., Dondera C.S., Deng J.M., Athama K., Ansari Y., A Chan M.M., Enlu A., Goldsmith A.D., Gurjal M., Hansen N.P., A Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M., Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawal J., A Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T., Satou M., Tamse R., Vaysberg M., Mallender E.K., Wong C., Yamamura Y., Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R., Theologis A., Ecker J.R., Theologis A., Ecker J.R.,
Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C., Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E., Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y., Kiyokawa C., Kohara M., Mateumoto M., Matsuno A., Muraki A., Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Tabata S.; "Sequence and analysis of chromosome 3 of the plant Arabidopsis thaliana."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PATHWAY: Nucleotide biosynthesis; IMP biosynthesis; 5-amino-1-(5-phospho-D-ribosyl)imidazole-4-carboxamide from N(2)-formyl-N(1)-(5-phospho-D-ribosyl)glycinamide: step 2.
SUBCELLUIAR LOCATION: Chloroplast.
SIMILARITY: Belongs to the AIR synthase family.
CAUTION: Ref. is sequence differs from that shown due to a frameshift in position 344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATALYTIC ACTIVITY: ATP + 2-(formamido)-N(1)-(5-phospho-D-ribosyl)acetamidine = ADP + phosphate + 5-amino-1-(5-phospho-D-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33.9%; Score 60; DB 1; Length 389; 42.1%; Pred. No. 21; tive 6; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ligase.
E341E9D21E9286F0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMBL; L12457; AAC37341.1; ALT_FRAME; Unassigned_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, AL132970; CAB82696.1; -; Genomic_DNA.
EMBL, AL049655; CAB41083.1; -; Genomic_DNA.
EMBL, AXV60585; AAL31210.1; -; mRNA.
EMBL, AXI40554; AAM98318.1; -; mRNA.
HSSP, P08178; 1CLI.
                                                                                                                                                                                       [3]
NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR010728; AIR_synth.
InterPro; IPR010918; AIR_synth_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             389 AA; 41504.MW;
                                                                                                                                                                Nature 408:820-822(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 302:842-846(2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ribosyl)imidazole.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      removed.
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RC MUDINE-2003408 PubMed=1067198, DOI=10.1038/47134;

REALINE-2003488 PubMed=1067198, DOI=10.1038/47134;

REALINE-2003488 PubMed=1067198, DOI=10.1038/47134;

RA MAPER X. Schueller C., Wambutt R., Murphy G., Volckaert G., Pohl T., Duesfechhoeft A., Stakekma W., Entian K.-D., Terryn N., Harris B., Amarcys W., Brandt P., Grivell L.A., Rieger M., Meichselgartner M., de Simone V., Obermaler B., Mache R., Mueller M., Reichert B., Portectella D., Perce-Alonso M., Boutry M., Bancroft I., Reichert B., Portectella D., Perce-Alonso M., Boutry M., Bancroft I., Reichert B., Portectella D., Perce-Alonso M., Boutry M., Bancroft I., Re Schuers J., Act R., Defoor E., Weltjean I., Voer P., Hobestel J., Zimmernann W., Wedler H., Ridley P., Defoor E., Reacken M., Weltjens I., Voer M., Bastiaens I., Aert R., Defoor E., Reacken M., Weltjens I., Voer M., Bastiaens I., Aert R., Defoor E., Reacken M., Weltjens I., Voer M., Bastiaens I., Aert R., Defoor E., Reicher B., Rempels S., Feldpeusch M., Hambert B., Rose M., Hauf J., Koetter P., Bernet B., S., Feldpeusch M., Lamberth S., Van den base H., De Keyser A., Buysshaert C., Gielen J., Villarroel R., De Clercq R., De Keyser J., Baysshaert C., Gielen J., Villarroel R., De Chercy R., Bose S., de Haan M., Marse A.C., Schaefer M., Mueller Auer S., Pettett A., Rajandream M., Lyne M., Benes V., Rechmann S., Argiriou A., Vitale D., Liguori R., Paravandi E., Massenet O., Quigley F., Clabauld G., Muenlein A., Felber R., Schmal S., Hiller R., Schmidt W., Erens W., Terol J., Torres A., Radobor P., Weber N., Vandembol M., Bargues M., Terol J., Torres A., Reibmann S., Argiriou A., Vitale D., Muenlein A., Felber S., Scholler P., Cooke R., Reas D., Seachust R., Reibmann D., Haase D., Lemck K., Hews H.-W., Stocker S., Reibmann D., Haase D., Lemck K., Hews H.-W., Stocker S., Scholler P., Cooker S., Scholler P., Cooker S., Prishman D., Haase D., Lemck K., Hews H.-W., Stocker S., Reibmann S., Scholler P., Cooker S., Scholler P., Cooker S., Scholler P., Cooker S., Scholler P., Cooker S., Scholler P., Seacar
RCCR ARAIn
QBLDT4; 023185;
10-00T-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 47, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21143384; PubMed=11149948; DOI=10.1073/pnas.021465298; Mach J.M., Castillo A.R., Hoogstraten R., Greenberg J.T.; "The Arabidopsis accelerated cell death gene ACD2 encodes red chlorophyll catabolite reductase and suppresses the spread of disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Molecular cloning, functional expression and characterization of RCC reductase, involved in chlorophyll catabolism.";
                                                                                                                                                                                          Name=RCCR; Synonyms=ACD2; OrderedLocusNames=At4g37000;
ORFNames=C7A10 360;
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Virialplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Aggnoliophyta; eudicotyledons; core eudicotyledons; cosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE, SUBCELLULAR LOCATION, AND MUTANTS ACD2-7;
                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE, FUNCTION, AND SUBCELLULAR LOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=cv. Columbia;
MEDLINE=20208062; PubMed=10743659;
Whith K.L., Bovet L., Hunziker P.E., Donnison I.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            roc. Natl. Acad. Sci. U.S.A. 98:771-776(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACD2-12E13 AND ACD2-6/ACD2-8.
STRAIN=cv. Columbia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plant J. 21:189-198(2000).
                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    reductase,
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Gaps

9

1 MESSLFSPSSSSYSSLFTAKPTR---LLSPKPKFTFSI 35 

Conservative

Local Similarity tes 16; Conserv

Best Loc Matches

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                                                                                                                                                                                                                                                                                                                                        STRAIN=CV. Columbia;

A MEDLINE=22954850; PubMed=14593172; DOI=10.1126/science.1088305;
A MEDLINE=22954850; PubMed=14593172; DOI=10.1126/science.1088305;
Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J., Cheuk R.P.,
A Miranda M., Quach H.L., Tripp M., Chang H.W., Turipp M., Chang M., Akiyama K., Ansari Y.,
A Chan M.M., Tang C.C., Donodera C.S., Deng J.M., Akiyama K., Ansari Y.,
A Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,
A Chao Q., Choy M., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,
A Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,
A Kamiya A., Meyers C., Nakajima M., Narusaka M., Sakurai T.,
Satou M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,
A Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;

"Empirical analysis of transcriptional activity in the Arabidopsis
Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D., Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K., Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.W., Nelson J., Spiech J., Ryan E., Andrews S., Geisel C., Layman D., Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshu C., Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C., Swaby I.K., O'Shaughnessy A., Rodriguez M., Metero A., Shah R., Swaby I.K., O'Shondy N., Hasegawa A., Hameed A., Lodhi M., Johnson A., Granat S., Shondy N., Hasegawa A., Hameed A., Lodhi M., Johnson A., Sequence and analysis of chromosome 4 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Full-length CDNA from Arabidopsis thaliana.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Catalyzes the key reaction of chlorophyll catabolism,
porphyrin macrocycle cleavage of pheophorbide a (pheide a) to a primary fluorescent catabolite (pFCC). Works in a two-step reaction with pheophorbide a oxygenase (PaO) by reducing the C20/CI double bond of the intermediate, RCC.
-!- COFACTOR: Reduced ferredoxin.
-!- COFACTOR: Reduced ferredoxin.
-!- PATHWAY: Chlorophyll degradation, fourth step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mitochondria of 7-day-old seedlings.
TISSUE SPECIFICITY: Expressed in all tissues tested, including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    change of levels during senescence or pathogen attack. MISCELLANEOUS: The absence of light completely suppresses cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chloroplast (Potential).
Red chlorophyll catabolite reductase.
Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AY093785; AAM10401.1; -; mRNA.
EMBL; AY085797; AAM63013.1; -; mRNA.
InterPro; IPRO09439; RCC_reductase.
Pfam; PF06405; RCC_reductase; Chlorophyll catabolism; Chloroplast; Coiled coil; Oxidoreductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEVELOPMENTAL STAGE: Present at all times of development. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
Broyer V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Z99707; CAB16763.1; -; Genomic DNA. AL161590; CAB80366.1; -; Genomic_DNA. AY045578; AAK73936.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF326347; AAG53980.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                death in acd2 mutants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genome.";
Science 302:842-846(2003).
                                                                                                                                                                                                                                                                            Nature 402:769-777(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                319
286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transit peptide
TRANSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brover V., Trou
Feldmann K.A.;
                                                                                                                                                                                                                                                            thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
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Galagan J.E., Calvo S.E., Borkovich K.A., Selker B.U., Read N.D.,

A Jaffe D., FitzHugh W., Man L.-J., Smirnov S., Purcell S., Rehman B.,

Bikins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,

Gui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,

A Selitrennikoff C.P., Kinsey J.A., Braun B.L., Zelter A., Schulte U.,

Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,

Koy A., Poley K., Naylor J., Thomann N., Barrett R., Gnerre S.,

Kamal M., Kamwysselis M., Mauceli E., Bielke C., Rudd S., Frishman D.,

Krystofowa S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,

Cogoni C., Macino G., Carcheside D., Li W., Pratt R.J., Osmani S.A.,

DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,

Arden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,

Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,

Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;

"The Genome Sequence of the Filamentous Fungus Neurospora crasss.";
G->V: In acd2-12E13; spontaneous spreading cell death lesions.
Missing: In acd2-7; spontaneous spreading cell death lesions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                    Gaps
                                                                279 R->K: In acd2-6; spontaneous spreading cell death lesions.
290 D -> E (in Ref. 5).
36449 MW; A46DC65FB7452517 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 which is
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                                                                                                                                                                                    3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neurospora crassa.
Eukaryota, Fungl; Ascomycota, Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
                                                                                                                                                   DB 1; Length 319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Length 624;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Indels
                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 0:0-0(2003).
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AABX11000213; EAA33018.1; -; Genomic_DNA.
SEQUENCE 624 AA; 65243 MW; 54F90D3DC736005C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                        æ
                                                                                                                                                                                                                       3 SSLFSPSSSSYSSLFTAKPTRL---LSPKPKF 31
                                                                                                                                                                                                                                          Match 33.3%; Score 59; DB Local Similarity 51.9%; Pred. No. 49; les 14; Conservative 4; Mismatches
                                                                                                                                                   33.6%; Score 59.5; D
43.8%; Pred. No. 19;
tive 7; Mismatches
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Q9VYN1;
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                                                                                                                                                                                        Conservative
      140
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NUCLEOTIDE SEQUENCE.
                                                                                                                        319 AA;
                                                                                                                                                                   Local Similarity
nes 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                              Predicted protein.
      140
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01-MAY-2000 (
01-OCT-2002 (
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RM WUCLECTIDE SEQUENCE.

RM WUCLECTIDE SEQUENCE.

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gacayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,

Radion R.C., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

Brandon R.C., Rogers Y.H.C., Blazej K.G., Change M., Pfeiffer B.D.,

RA Burlu J.F., Agbayani A., An H.-J., Andrews-Ffannkoch C., Baldwin D.,

RA Ballaw R.M., Basu A., Baxendale J., Bayraktarolo, Bolbhakov S.,

RA Burli J.F., Agbayani A., An H.-J., Andrews-Ffannkoch C., Baldwin D.,

RA Burli J.F., Agbayani A., Buller H., Cadieu E., Center A., Chandra I.,

RA Burlis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

RA Burlis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

RA Burlis K.C., Busam D.A., Ballke C., Davenport L.B., Davies P.,

RA Ge Pablos B., Delchar A., Deng Z., Mays A.D., Davies P., Andrews P.,

RA Gerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Harris N.L., Barogalista C.C., Ferraz C., Ferriacz S., Dunkov B.C.,

RA Harris N.L., Harvey, D.A., Heiman T.J., Harnandez J.R., Houck J.,

RA Harris N.L., Malush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Harris N.L., Malush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Harris N.L., Malush F., Karpen G.H., Ke Z., Kennison J.A., Malton B.E., Kodira C.D., Kraft C., Mcris J., Welmel B.E.,

Randl M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Melson D.L.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Wosherin A.,

Rander S.M., Moy M., Murphy B., Murphy L., Mursh, Merkulov G., Milshina N.V., Nison K. D., Wolsker E., Wang X.,

Reiner K., Peters G., Standers R.D.C., Scheeler F., Shen H.,

Shue B.C., Siden-Klamos I., Simpson M., Strong R., Welsenbach J.,

Rander S.M., Woodage T., Stangen G.M., Weisenbach J.,

Rander S.M., Woodage T., Stangen G.M., Weisenbach J.,

Rander S.M., Woodage T., Stangen G.M., Weisenbach J.,

Rander S.M., Woodage T., Stan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin: a genomics perspective.";
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BUDILNE-SZ426069; PubMed=12537572;

Misra S., Croeby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,

Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.B.
Name=CG11245; ORFNames=CG11245;
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3enome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002)
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NUCLEOTIDE SEQUENCE.
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STRAIN=C57BL/6N; TISSUB=Testis;
Ban N., Sasaki M., Sakai H., Uded K., Inagaki N.;
"Cloning of ABCA17, a novel rodent sperm-specific ABC (ATP-binding
cassette) transporter that regulates intracellular lipid metabolism.";
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P., Bettencourt B.R., Celliker S.E., de Grey A.D., N.J., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
                                                                                                                                                                                                                                                                 Berkeley Drosophila Genome Project,
Celniker S., Carlson J., Wan K., Pfeiffer B., Frise B., George R.,
Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                          Lewis S.E.; "Annotation of the Drosophila melanogaster euchromatic genome:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 59; DB 2; Length 1545;
Pred. No. 1.4e+02;
3; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1733;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE003489; AAF48161.1; -; Genomic_DNA.
Ensembl; CG11245; Drosophila melanogaster.
Flybase; Psyn0030388; CG1128; CSTCS45;
SEQUENCE 1545 AA; 166082 MW; 2ABCEABED136C8B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1733 AA; 195943 MW; 2D4DB5BBD19F6D6E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                         "Drosophila melanogaster release 4 sequence.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                    Genome Biol. 3: RESEARCH0083.1-RESEARCH0083.22 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
ATP-binding cassette (ABC) transporter ABCA14.
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Pred. No. 1.6e+02;
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Biochem. J. 389:577-585(2005).
EMBL, Pall2584; BAD97416.1; -; mRNA.
ATP-binding.
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Best Local Similarity 44.1%;
Matches 15; Conservative
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                                                                                                                                                            review.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAR-2005)
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                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                             fu C., Rubin G.;
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ID Q1
AC Q1
DT 01
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GO; GO:0008152; P:metabolism; IEA.
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                                                                                                                                                                Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99069613; PubMed=9851916; DOI=10.1126/science.282.5396.2012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ensembl; T09F3.1; Caenorhabditis elegans.

R WormBase; WBGene00011661; T09F3.1.

R WormBep; T09F3.1; CaE35906.

R GO; GO:0005634; Cinucleus; IEA.

GO; GO:0003676; Finecal ion binding; IEA.

GO; GO:0003775; Finecal ion binding; IEA.

GO; GO:0007775; Pievelopment; IEA.

R R GO; GO:00096; ZICC2H2; 1.

R SMART; SM00355; ZIR C2H2; 2.

R ROSITE; PS50157; ZINC_FINGER_C2H2_1; UNKNOWN_1.

R PROSITE; PS50157; ZINC_FINGER_C2H2_1; UNKNOWN_1.

R PROSITE; PS50157; ZINC_FINGER_C3H2_2; 1.

R Metal-binding; Nuclear protein; Zinc; Zinc-finger.

O SEQUENCE 355 AA; 39236 WW; 56B98564B2926062 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chamaecyparis obtusa (Japanese cypress).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Coniferopsida, Coniferales, Cupressaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Katch S., Hyatt D., Ogawa K., Fujii M., Furuno T., Croteau R.; Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AB120957; BAC92722.1; -; mRNA.
GO; GO:001689; F:lyase activity; IEA.
GO; GO:000287; F:lyase activity; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                The C. elegans sequencing consortium; "Genome sequence of the nematode C. elegans: a platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O9TZ38:gei-4; NDEXp=1; IntAct=EBI-329146, EBI-329192; G9U9Y8:lit-1; NDExp=1; IntAct=EBI-329146, EBI-318513; EMBL; Z49908; CAA90104.2; -; Genomic_DNA. EMBL; Z49070; CAA88872.2; -; Genomic_DNA. EMBL; Z49070; CAA8872.2; -; Genomic_DNA. EMBL; Z49070; CAA8872.2; JOINED; Genomic_DNA. EMBL; Z49070; CAA88872.2; JOINED; Genomic_DNA. EMBL; Z490793; CAA8872.2; JOINED; Genomic_DNA. EMBL; Z490793; CAA8872.2; JOINED; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 SSLFSPSSSS----YSSLFTAK---PTRLLSPKPKFTFS 34
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Last annotation update)
      01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
Hypothetical protein T09F3.1.
ORFNames-T09F3.1.
                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     605 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33.1%; Score 58.5; D
46.2%; Pred. No. 30;
tive 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   investigating biology.";
Science 282:2012-2018(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Limonene/borneol synthase. Name=col;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q75W1_CHAOB PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 46.2
nes 18; Conservative
                                                                                                                                  Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                       STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=13415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- INTERACTION:
                                                                                                                                                                                                                                          NCBI_TaxID=6239;
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O75WM1 CHA
ID O75WM
AC 075WM
DT 05-JT

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Sucgang R., Bertiman M., Song J., Olsen R., Szafranski K., Xu Q.,
Sucgang R., Bertiman M., Song J., Olsen R., Szafranski K., Xu Q.,
Tunggal B., Kummarefeld S., Madera M., Konfortov B.A., Rivero F.,
Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
Rerbornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
Rerbortour P., Desany B., Just E., Morio T., Rost R., Churcher C.,
Rarborther P., Desany B., Just E., Morio R., Churcher C.,
Ruzny D., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
Hauser H., James K., Ouiles M., Mohan M.B., Saito T., Buchrieser C.,
Rardroper A., Felder M., Thangavelu M., Johnson D., Knights A.,
Loulseged H., Mungall K., Oliver K., Price C., Quall M.A.,
Nuchihara H., Hernandez J., Rabbinowitsch E., Steffen D., Sanders M.,
Na J., Kohara Y., Sharp S., Simmonds M., Spiegler T., Tanaka Y.,
Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
Shaulsky G., Schleicher M., Weinstock G., Rosenthal A., Cox E.C.,
Chisholm R.L., Gibbs R., Loomis W.F., Riatzer M., Kay R.R.,
Williams J., Doar P.H., Noegel A.A., Barrell B., Kuspa A.;
Nature O.O-O(2005).
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DictyBase; DDB0216197; Pde4.
DictyBase; DDB0216197; Pde4.
GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.
GO; GO:0015787; F:hydrolase activity; IEA.
GO; GO:0007165; P:signal transduction; IEA.
InterPro; IPR003607; Met_phos_hydro.
InterPro; IPR002073; PDEase.
                                                                                                                                                                                                                                                                                                 Gaps
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01-JTN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Putative cyclic nucleotide phosphodiesterase (Hypothetical protein
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                                                                                                                                                                                                                 DB 2; Length 605; 64;
                                                                                                                                                                                                                                                                                                 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bader S., Van Haastert P.J.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases
                                                                Pfam; PPO1397; Terpene Synth; 1.
Pfam; PPO3936; Terpene Synth C; 1.
SEOURNCE 605 AA; 70309 MW; CE4DD12D6A4462F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein.
SEQUENCE 771 AA; 88908 MW; 2036F7D8DC9D6E07 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=Pde4; ORFNames=DDB0216197;
Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AY211984; AAO59486.1; -; mRNA.
EMBL; AAFI01000196; EAL62868.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32.8%; Score 58; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  771 AA
                                                                                                                                                                                                                                                                                              5; Mismatches
                                                                                                                                                                                                                 Query Match 32.8%; Score 58; Best Local Similarity 44.4%; Pred. No. (Matches 12; Conservative 5; Mismatch
                                                                                                                                                                                                                                                                                                                                                                          4 SLFSPSSSSYSSLFTAKPTRLLSPKPK 30
                                                                                                                                                                                                                                                                                                                                                                                                                    2 ALISESSAFTFCLKSKPTHLSKPSPK 28
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InterPro; IPR005630; Terpene_synth_C.
InterPro; IPR001906; Terp_synth-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00387; PDIESTERASE1.
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Q86H13 DICDI
ID Q86H13 DICDI PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=44689;
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0; Gaps Best Local Similarity 51.9%; Pred. No. 85; Matches 14; Conservative 2; Mismatches 11; Indels

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8 PSSSSYSSLFTAKPTRLLSPKPKFTFS 34

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Search completed: March 7, 2006, 21:58:12 Job time : 181.2 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

March Run on:

7, 2006, 21:59:17; Search time 140.4 Seconds (without alignments) 107.136 Million cell updates/sec

Title: Perfect score:

US-10-751-235-11 177 1 MESSLFSPSSSSYSSLFTAKPTRLLSPKPKFTFSIR 36 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1867569 segs, 417829326 residues Searched:

1867569 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published Applications AA Main: \*

1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep: \*

2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep: \*

2: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep: \*

3: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep: \*

5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep: \*

6: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep: \*

6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	g		11, Appl	4, Appli	6317, Ap	688, App	601, App	vo	18525, A	5867, Ap	5866, Ap	348345,	230527,	57, Appl	57, Appl	5731, Ap	260318,	23523, A	278783,	257160,	257159,	257153,	201457,	261750,	236698,	35222, A	196060,		245828,
	Description		Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
SUMMARIES	QI.		US-10-751-235-11	US-10-751-235-4	US-10-739-930-6317	US-10-310-154-688	US-10-732-923-601	US-10-732-923-21136	US-11-097-143-18525	0-732-923	US-10-732-923-5866	US-10-425-115-348345	US-10-424-599-230527	US-09-870-406A-57	US-10-159-901-57	US-10-739-930-5731	US-10-424-599-260318	1-097-	US-10-424-599-278783	US-10-425-115-257160	US-10-425-115-257159	US-10-425-115-257153	-10-424-599	7	-424-599	-10-450-763	-10-424-599	-11-097-143-	US-10-424-599-245828
	DB	1	Ŋ	Ŋ	Ŋ	4	'n	Ŋ	9	'n	Ŋ	4	4	m	4	'n.	4	9	4	4	4	4	4	4	4	'n	4	9	4
	Query Match Length	- 1	36	539	260	260	260	262	2016	.309	424	82	389	319	319	319	525	1545	78	109	131	160	215	283	. 131	48	204	883	370
مه	Query		100.0	100.0	100.0	35.6	35.6	'n	35.3	34.7	34.7	34.5			•	ë.	33.6	33.3	33.1	32.8	32.8	32.8	32.5	32.5	•	•	ij	31.6	31.4
	Score		177	177	177	63	63	63	62.5	61.5	61.5	61	ø	59.5	59.5	٠	on	29	58.5	28	58	28	57.5	57.5	56.5	96	26	26	55.5
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	218604,	196064,	159373,	188070,	191224,	147306,	158653,	2, Appli	1314, Ap	1459, Ap	194264,	2, Appli	256870,	224645,	21141, A	265695,	8, Appli
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
US-10-425-114-37736	US-10-424-599-218604	US-10-424-599-196064	US-10-424-599-159373	US-10-424-599-188070	US-10-424-599-191224	US-10-424-599-147306	US-10-424-599-158653	US-10-498-428-2	US-10-374-780A-1314	US-10-412-699B-1459	US-10-424-599-194264	US-10-234-961-2	US-10-424-599-256870	US-10-424-599-224645	US-10-732-923-21141	US-10-424-599-265695	US-10-094-458A-8
4	4	4	4	4	4	4	4	Ŋ	4	4	4	4	4	4	ß	4	4
370	206	97	116	246	254	282	741	1536	416	416	527	2027	87	167	170	195	205
31.4	31.4	31.1	31.1	31.1	31.1	31.1	31.1	31.1	30.8	30.8	30.8	30.8	30.5	30.5	30.5	30.5	30.5
55.5	55.5	55	25	55	22	55	52	. 22	54.5	54.5	54.5	54.5	54	54	54	54	54
28	53	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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APPLICANT: Tian, Li
APPLICANT: Tian, Li
APPLICANT: Tian, Joonyul
TITLE OF INVENTION: Novel Carotenoid Hydroxylases for Use in Engineering Carotenoid
TITLE OF INVENTION: Metabolism in Plants
FILE REFERENCE: MSU-08604
CURRENT APPLICATION NUMBER: US/10/751,235
CURRENT FILING DATE: 2004-01-02
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
LENGTH: 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 177; DB 5; Best Local Similarity 100.0%; Pred. No. 1e-15; Matches 36; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MESSLFSPSSSSYSSLFTAKPTRLLSPKFKFTFSIR 36
Sequence 11, Application US/10751235
Publication No. US20050150002A1
GENERAL INFORMATION:
APPLICANT: DellaPenna, Dean
                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-751-235-11
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1 MESSLFSPSSSYSSLFTAKPTRLLSPKPKFTFSIR 36 US-10-751-235-4 셤

APPLICANT: Tian, Li
APPLICANT: Tian, Li
APPLICANT: Kim, Joonyul
TITLE OF INVENTION: Novel Carotenoid Hydroxylases for Use in Engineering Carotenoid
TITLE OF INVENTION: Metabolism in Plants
FILE REFERENCE: MSU-08604
CURRENT APPLICATION NUMBER: US/10/751,235
CURRENT FILING DATE: 2004-01-02
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PatentIn version 3.2
SEQ ID NO 4
LENGTH: 519
TYPE: PRT Sequence 4, Application US/10751235
Publication No. US2005015002A1
GENERAL INFORMATION:
APPLICANT: DellaPenna, Dean

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APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: TRANGENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REFERENCE: 38-15(52796)C
CURRENT APPLICATION NUMBER: US/10/732,923
CURRENT FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: 10/310,154
PRIOR APPLICATION NUMBER: 10/310,154
NUMBER OF SEQ ID NOS: 24149
SEQ ID NO 601
                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Gene Sequences and Uses Thereof in Plants FILE REFERENCE: 38-15(52796)B
CURRENT APPLICATION NUMBER: 08/10/310,154
CURRENT FILING DATE: 2002-12-04
PRIOR PAPLICATION NUMBER: 60/337,358
PRIOR PILING DATE: 2001-12-04
NUMBER OF SEQ ID NOS: 736
SEQ ID NO 688
LENGTH: 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 35.6%; Score 63; DB 4; Length 260; Best Local Similarity 46.2%; Pred. No. 5.7; Matches 12; Conservative 6; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 260;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35.6%; Score 63; DB 5; 46.2%; Pred. No. 5.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 SATSASLFSANPTPLFSPKPSLSLHL 29
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; Publication No. US20050108791A1
; GENERAL INFORMATION:
Lund, Adrian Madson, Linda L. Malloy, Kathleen A. McKlel, Christine L. Miller, Philip W. Padmavathi, Manchikanti Parnell, Laurence D. Start, William G. Tennesen, Dan Vidya, K.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 601, Application US/10732923
Publication No. US20050108791A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                               Yang, Chunzhi
Zeng, Xiaoping
Zhang, Qiang
Zhao, Yajuan
Zhou, Li
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Best Local Similarity 46.2
Matches 12; Conservative
                                                                                                                                                                                                                                         Xin, Zhanguo
Xu, Nanfei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
CORGANISM: Glycine max
US-10-732-923-601
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                                                                                           APPLICANT
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Squence 6317, Application US/10739930
Squence 6317, Application US/20040216190A1
Squence 6317, Application US/20040216190A1
Squence 6317, Application US/20040216190A1
GREEAL INFORMATION:
TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
TITLE OF INVENTION: US/10/739,930
CURRENT FILING DATE: 2003-12-18
SEQ ID NO 6317
LENGTH: 560
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                                                                       Length 539;
                                                                                                                 Indels
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                                                                       100.0%; Score 177; DB 5; 100.0%; Pred. No. 2.1e-14;
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                                                                                                                                                         1 MESSLFSPSSSSYSSLFTAKPTRLLSPKPKFTFSIR 36
                                                                                                                                                                                    1 MESSLFSPSSSSYSSLFTAKPTRLLSPKPKFTFSIR 36
                                                                                                                 0; Mismatches
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Publication No. US20030233670A1
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Laccetti, Lucille B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Boddupalli, Raghava
Deikman, Jill
Deng, Molian
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Johnson, G. Richard
Jung, Vincent
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Galligan, Meghan M.
Hinchey, Brenda S.
        ; ORGANISM: Arabidopsis thaliana US-10-751-235-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Agarwal, Ameeta K.
Ahrens, Jeffrey E.
Ball, James A.
Banu, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Edgerton, Michael D
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Adams, Thomas H
Ruff, Thomas G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ai, Chao-Qiang
                                                                     Query Match
Best Local Similarity 100.0
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36; Conservative
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iu, Jingdong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , Jinzhuo
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GENERAL INFORMATION:
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APPLICANT:
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Gaps

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Sequence 5866, Application US/10732923

Publication No. US20050108791A1

GENERAL INFORMATION:

APPLICANT Edgerton, Michael D

TITLE OF INVENTION: TANGEBLE US/10/732,923

FILE REFERENCE: 38-15(52796) C

CURRENT FILING DATE: 2003-12-10

PRIOR FILING DATE: 2003-12-04

NUMBER OF SEQ ID NOS: 24149

SEQ ID NO 5866

LENGTH: 424
                                                      Sequence 5867, Application US/10732923
Publication No. US20050108791A1
GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D
ITILE OF INVENTION:
PILE REPREBENCE: 38-15(52796)C
CURRENT FILING DATE: 2003-12-10
PRIOR PLICATION NUMBER: 10/310,154
PRIOR PLICATION NUMBER: 10/310,154
PRIOR PLICATION NUMBER: 10/310,154
PRIOR PLICATION DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 24149
SEQ ID NO S867
LENGTH: 309
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43.8%; Pred. No. 11;
tive 6; Mismatches 11;
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Pred. No. 15;
6; Mismatches 11;
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i OTHER INFORMATION: unsure at all Xaa locations
US-10-732-923-5867
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NAME/KEY: unsure

LOCATION: (1)..(424)

CHER INFORMATION: unsure at all Xaa locations
US-10-732-923-5866
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Publication No. US20040214272A1
GENERAL INFORMATION:
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Best Local Similarity 43.8%;
Matches 14; Conservative
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Triticum aestivum
FEATURE:
NAME/KEY: unsure
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 43.8
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
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APPLICANT: VENTER: J. CYA19

TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: DROSOPHILA GENES.

TITLE OF INVENTION: DROSOPHILA GENES.

TITLE OF INVENTION: DROSOPHILA GENES.

CURRENT APPLICATION NUMBER: US/11/097,143

CURRENT APPLICATION NUMBER: 60/150,191

PRIOR APPLICATION NUMBER: 60/160,191

PRIOR APPLICATION NUMBER: 60/160,191

PRIOR APPLICATION NUMBER: 60/160,191

PRIOR PILING DATE: 1999-10-19

PRIOR PILING DATE: 1999-11-12

PRIOR PILING DATE: 1999-11-2

PRIOR PILING DATE: 2000-02-24

PRIOR PILING DATE: 2000-02-24

PRIOR PILING DATE: 2000-02-24

PRIOR PILING DATE: 2000-03-23

NUMBER OF SEQ ID NOS: 41008

SCOTTANARE: RESESSED FOR WINDOWN VERSION 4.0
APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REPERENCE: 38-15/52796/C
CURRENT APPLICATION NUMBER: US/10/732,923
CURRENT FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: 10/310,154
PRIOR PLING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 24149
SEQ ID NO 21136
LENGTH: 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 262;
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Pred. No. 5.8;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                       i LOCATION: (1)..(262)
i OTHER INFORMATION: unsure at all Xaa locations
US-10-732-923-21136
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Pred. No. 65;
4; Mismatches
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Publication No. US20050208558A1
GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
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Best Local Similarity 46.2%;
Matches 12, Conservative
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Best Local Similarity 47.4º
Matches 18; Conservative
                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                           PEATURE:
NAME/KEY: unsure
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Gaps

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APPLICANT: KOICHI, TAKAYUKI
APPLICANT: FRANKENBERG, NICOLE
APPLICANT: FRANKENBERG, NICOLE
APPLICANT: GAMBETTA, GREGORY
APPLICANT: GAMBETTA, GREGORY
APPLICANT: GAMBETTA, GREGORY
APPLICANT: MONTGOWERY, BERRONDA
TITLE OF INVENTION: LIGHT CONTROLLED GENE EXPRESSION UTILIZING HETEROLOGOUS PHYTOCHRON
FILE OF INVENTION: 1 LIGHT CONTROLLED GENE EXPRESSION UTILIZING HETEROLOGOUS PHYTOCHRON
CURRENT PREZERORICE: 4077-207731US
CURRENT PELING DATE: 2002-05-29
FRIOR APPLICATION NUMBER: 60/294,463
FRIOR PILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 57
SOFTWARE: Patentin version 3.0
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Publication No. US20040216190A1

GENERAL INFORMATION:
PAPLICANT: Kovalic, David K.
TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT

TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT

TITLE OF INVENTION: US 10377) B

CURRENT APPLICATION NUMBER: US/10/739,930

CURRENT FILING DATE: 2003-12-18

SEQ ID NO 5731

LENGTH: 319
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US-10-739-930-5731
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7 NTLYSSSSPSYLSPLTSKPSRFSKNLRPRAQF 38
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Best Local Similarity 43.8%; Pred. No. 20;
Matches 14; Conservative 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                           7; Mismatches
                                                                                                                                                                                                                                                                                                   Score 59.5;
Pred. No. 20
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Publication No. US20030073235A1
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ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Arapidopsis thaliana
US-10-159-901-57
                                                                                                                                                         TYPE: PRT
ORGANISM: Arapidopsis thaliana
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Best Local Similarity 43.8%;
Matches 14; Conservative
       NUMBER OF SEQ ID NOS: 57
SOFTWARE: Patentin version 3.0
SEQ ID NO 57
LENGTH: 319
                                                                                                                                                                                                                                                                                                       Query Match 33.6%;
Best Local Similarity 43.8%;
Matches 14; Conservative
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APPLICANT: LAGARIAS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-739-930-5731
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Sequence 230527, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Cao Yonowei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE SEPERENCE: 38-21(53233)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 230527

LENGTH: 389
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants
FILE REPERBENCE: 38-21(53.22)8
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 348345
LENGTH: 82
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46.9%; Pred. No. 16;
tive 4; Mismatches 13; Indels
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Pred. No. 2.9;
6; Mismatches 7; Indels
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FUBLICATION O. US20030104379A1
GENERAL INFORMATION:
APPLICANT: LAGARIAS, JOHN
APPLICANT: KOICHI, TAKAYUKI
APPLICANT: FRANKENBERG, NICOLE
APPLICANT: GAMBETTA, GREGONY
APPLICANT: GAMBETTA, GREGONA
TITLE OF INVENTION: HY2 FAMILY OF BILIN REDUCTASES
FILE REFREENCE: 407T-9072208
CURRENT APPLICATION NUMBER: US/09/870,406A
CURRENT PILING DATE: 2002-09-04
FRIOR APPLICATION NUMBER: 60/211,758
PRIOR FILING DATE: 2001-02-26
FRIOR APPLICATION NUMBER: 60/210,286
FRIOR FILING DATE: 2000-06-08
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US-10-424-599-230527
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US-10-425-115-348345
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Best Local Similarity 43.5%;
Matches 10; Conservative
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Matches 15, Conservative
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ORGANISM: Glycine max
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US-09-870-406A-57
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Sequence 26018, Application US/10424599

Publication No. US20040031072A1

Publication No. US20040031072A1

Publication No. US20040031072A1

APPLICANT: La Rosa Thomas J

APPLICANT: Kovalto David K

APPLICANT: Acou Yihua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53223)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 260318

LENGTH: 525

TWOPD: NOW
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_77090C.1.pep

US-10-424-599-260318
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NAME/KEY: ungure
LOCATION: (1)..(525)
OTHER INFORMATION: ungure at all Xaa locations
TYPE: PRT
ORGANISM: Glycine max
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Search completed: March 7, 2006, 22:04:14 Job time : 140.4 secs

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US-10-839-227-129
US-10-839-673-1595U
US-10-351-641-487
US-10-351-641-489
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US-10-351-641-489
US-10-351-641-499
US-10-351-641-499
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US-10-425-115-314843
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/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
       GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
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US-10-210-965-5

US-10-236-433-11

US-10-236-433-11

US-10-477-526-7

US-10-477-526-7

US-10-751-235-14

US-10-751-235-14

US-10-751-235-15

US-10-373-877-10

US-10-373-877-20

US-10-373-877-21

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US-10-926-683-1257
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                                                                                                                                              1867569 segs, 417829326 residues
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Maximum Match 100%
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40.0%; Pred. No. 3.5e+02;
tive 6; Mismatches 0; Indels
Sequence 129, Application US/09739254

Sequence 129, Application US/09739254

Batent No. US20010021700A1

GENERAL INFORMATION:

APPLICANT: ROSEN et al.

TITLE OF INVENTION: 49 Human Secreted Proteins
FILE REFRENCE: P2032P1

CURRENT APPLICATION NUMBER: US/09/739,254

CURRENT FILING DATE: 2000-02-23

EARLIER PILING DATE: 2000-02-23

EARLIER APPLICATION NUMBER: 60/097,917

EARLIER FILING DATE: 1998-08-24

EARLIER FILING DATE: 1998-08-25

EARLIER FILING DATE: 1998-08-25

EARLIER FILING DATE: 1998-08-31

NUMBER OF SEQ ID NOS: 170

SOFTWARE: PATENTI VET. 200

SOFTWARE: PATENTI VET. 200

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SOFTWARE: PATENTI VET. 200
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Patent No. US20020026040A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 49 Human Secreted Proteins
FILE REFERENCE: PZ032P1
CURRENT APPLICATION NUMBER: US/09/904,615
CURRENT APPLICATION NUMBER: 09/511,554
PRIOR PILING DATE: 2000-02-23
PRIOR PILING DATE: 1998-08-25
PRIOR PILING DATE: 1998-08-25
PRIOR PILING DATE: 1998-08-25
PRIOR PILING DATE: 1998-08-25
PRIOR PILING DATE: 1998-08-11
NUMBER OF SEC ID NOS: 170
SOFTWARE: Patentin Ver. 2.0
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CORGANISM: Homo sapiens
US-09-904-615-129
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ORGANISM: Homo sapiens
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RESULT 3

US-10-067-534-15

Sequence 15, Application US/10067534

Publication No. US20020187538A1

GENERAL INFORMATION:
APPLICANT: Essenberg, Margaret K.
APPLICANT: Duo, Ping
APPLICANT: Luo, Ping
APPLICANT: OF INGENICANT Cons. Cons. (+) -Delta-Cadinene-8-Hydroxylase Gene from Cotton Fill Correst APPLICANT: Wang, Yan-Hong
APPLICANT: OF INS. 105-07
BRIOR APPLICATION NUMBER: US 60/267,160
PRIOR APPLICATION NUMBER: 2002-02-07
PRIOR FILING DATE: 2001-02-07

NUMBER OF SEQ ID NOS: 19
SOFTWARE: PastSEQ for Windows Version 4.0

LENGTH: 10
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; Bequence 5, Application US/10210965
; Publication No. US200300744041
; GENERAL INFORMATION:
    APPLICANT: Glucksmann, Maria A.
; TITLE OF INVENTION: Member and Uses Therefor
; FILE REPRENCE: MPIO1-091PIRM;
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US/10/210,965
; PRIOR APPLICATION NUMBER: 60/312428
; RIOR PILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 6
; SOF ID NOS: 6
; SEQ ID NO 5
; SEQ ID NO 5
; LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 33; DB 4; Length 10; 40.0%; Pred. No. 3.5e+02;
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LOCATION: 5
OTHER INFORMATION: Xaa can be any amino acid.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 3.56
6; Mismatches
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OTHER INFORMATION: Ser can be Gly, Asn, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 1
O'THER INFORMATION: Phe can be Trp.
PEATURE:
NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  can be Asp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Gossypium arboreum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 FXXGXXXCXG 10
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1 FGSGRRMCAG 10
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LOCATION: 4
OTHER INFORMATION: Gly
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Best Local Similarity
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NAME/KEY: VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-067-534-15
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APPLICANT: Ramshaw, Heather
APPLICANT: Remshaw, Heather
TITLE OF INVENTION A Retinoic Acid Metabolizing Cytochrome P450
FILE REFERENCE: 11812-91
CURRENT FILING DATE: 2003-11-21
PRIOR APPLICATION NUMBER: US 60/292,531
PRIOR PILING DATE: 2001-05-24
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Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 10; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 33; DB 4; I
100.0%; Pred. No. 3.5e+02;
TITLE OF INVENTION: Insecticide Targets
FILE REFERENCE: 09531-070001
CURRENT APPLICATION NUMBER: US/10/236,433
CURRENT FILING DATE: 2002-12-10
FRIOR APPLICATION NUMBER: 60/318,006
FRIOR APPLICATION NUMBER: 60/317,890
FRIOR FILING DATE: 2001-09-07
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version, 4.0
SEQ ID NO 11
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                           NAME/KEY: VARIANT
CACATION: 2,3,5,6,7,9
COTHER INFORMATION: Xaa = Any Amino Acid
US-10-236-433-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/10477526
Publication No. US2005009021A1
GENERAL INFORMATION:
APPLICANT: Wisniewski, Jan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: MISC FEATURE
LOCATION: (9). (9)
OTHER INFORMATION: x=any residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: MISC_FEATURE
LOCATION: (5)...(7)
CTHER INFORMATION: x=any residue
US-10-477-526-7
                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                         OTHER INFORMATION: P450 motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin version 3.1
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (2)...(3)
OTHER INFORMATION: x=any
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 FXXGXXXCXG 10
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NAME/KEY: MISC FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                    NAME/KEY: VARIANT
LOCATION: (9)...(9)
JTHER INFORMATION: Leu can be Ile, Val, Met, Phe, Ala, or Pro.
                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 33; DB 4; Length 10; 70.0%; Pred. No. 3.5e+02; Live 3; Mismatches 0; Indels
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.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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                                                                                                                                          WANE/KEY: VARIANT
LOCATION: (8)...(8)
OTHER INFORMATION: Cys is involved in binding heme iron
                    OCATION: (6)...(6)
MHER INFORMATION: Arg can be Lys, His, Pro, or Thr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: VARIANT
LOCATION: (7)...(7)
OTHER INFORMATION: Xaa can be any amino acid.
                                                                                                                                                                                                                                                                               ; NAME/KEY: VARIANT
; LOCATION: (10) ...(10)
; OTHER INFORMATION: Gly can be Ala or Asp
US-10-210-965-5
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Publication No. US20030100025A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.
Best Local Similarity 70.0
Matches 7; Conservative
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Best Local Similarity 40.0
Matches 4; Conservative
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1 FSXGXRXCLG 10
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FSLGRRHCLG 10
   VARIANT
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APPLICANT: Tian, Li
APPLICANT: Tian, Li
APPLICANT: Tian, Li
APPLICANT: Tian, Li
APPLICANT: Tian, Lonyul
TITLE OF INVENTION: Novel Carotenoid Hydroxylases for Use in Engineering Carotenoid
TITLE OF INVENTION: Metabolism in Plants
FILE REFERENCE: MSU-08604
CURRENT APPLICATION NUMBER: US/10/751,235
CURRENT FILING DATE: 2004-01-02
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin version 3.2
SEQ ID NO 15
ELENGTH: 10
TYPE: PRT
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US-10-097-559-28

Sequence 28, Application US/10097559

Publication No. US2030166255A1

GRENERAL INFORMATION,

APPLICANT: Chappell,

TITLE OF INVENTION: Cytochrome P450s and Uses Thereof

FILE REPERENCE: 07678/100003

CURRENT APPLICATION NUMBER: US/10/097,559

CURRENT FILING DATE: 2002-03-08

PRIOR PILLING DATE: 2001-03-09

PRIOR APPLICATION NUMBER: US 60/274,241

PRIOR APPLICATION NUMBER: US 60/275,597

PRIOR PILLING DATE: 2001-03-03

NUMBER: OF SEQ ID NOS: 43

SOFTWARE: FASTERO FOR WINDOWS VERSION 4.0

LENGTH. 11
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100.0%; Score 33; DB 5;

Best Local Similarity 40.0%; Pred. No. 3.5e+02;

Matches 4; Conservative 6; Mismatches 0
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ORGANISM: Nicotiana tabacum p450 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 4,8
COTHER INFORMATION: Xaa = Any Amino Acid
US-10-097-559-28
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US-10-804-772-26
; Sequence 26, Application US/10804772
                                                                                              RESULT 10
US-10-751-235-15
Sequence 15, Application US/10751235
Publication No. US20050150002A1
GENERAL INFORMATION:
APPLICANT: PollaPenna, Dean
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60.0%; F
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US-10-751-235-15
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Best Local Similarity 60.0
Matches 6; Conservative
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2 FGXGRRXCPG 11
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1 FSGPRKCVG 10
1 FXXGXXXCXG 10
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US-10-51-235-14

Sequence 14, Application US/10751235

Sequence 14, Application No. US20050150002A1

GENERAL INFORMATION:
APPLICANT: DellaPenna, Dean
APPLICANT: Tian, Li
APPLICANT: Kim, Joonyul
TITLE OF INVENTION: Novel Carotenoid Hydroxylases for Use in Engineering Carotenoid
TITLE OF INVENTION: Metabolism in Plants
FILE REFERENCE: MSU-08604

CURRENT APPLICATION NUMBER: US/10/751,235

CURRENT PILING DATE: 2004-01-02

NUMBER OF SEQ ID NOS: 74

SOUTWARE: PatentIn version 3.2

LENGTH: 10

LENGTH: 10
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NAME/KEY: misc_feature

LOCATION: (9)...(9)

OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-751-235-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature
LOCATION: (5). \( (7)\)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
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LOCATION: (2). 7(3)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
                                                                                                                                                                       APPLICANT: Wishinski, Jan
APPLICANT: Wanniewski, Jan
APPLICANT: Ramshaw, Heather
APPLICANT: Ramshaw, Heather
APPLICANT: Retwortch, Martin P.
TITLE OF INVENTION: A Retinoic Acid Metabolizing Cytochrome P450
FILE REFERENCE: 11812-91
FILE REFERENCE: 11812-91
FURNERT FILING DATE: 2003-11-21
PRIOR APPLICATION NUMBER: US 60/292,531
RHOR FILING DATE: 2010-62-24
NUMBER: OF SEQ ID NOS: 29
SOFTWARE: PatentIn version 3.1
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Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                   ; Sequence 8, Application US/10477526
; Publication No. US20050009021A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Conservative
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1 FGGGARSCLG 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-477-526-8
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Length 11;

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Query Match
Best Local Similarity
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                                                                                           Matches
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                                                                          APPLICANT: Choe, Sunghwa
APPLICANT: Choe, Sunghwa
APPLICANT: Peldmann, Kenneth A.
TITLE OF INVENTION DWF4 POLYNUCLEOTIDES, POLYPEPTIDES AND USES THEREOF
FILE REPERBUCE: 11696-070001
CURRENT APPLICATION NUMBER: US/10/804,772
CURRENT APPLICATION NUMBER: US/09/502,426
PRIOR PELING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: US 60/119,657
PRIOR PILING DATE: 1999-02-11
PRIOR PELING DATE: 1999-02-11
PRIOR PLILING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SSOFTWARE: RastSEQ for Windows Version 4.0
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APPLICANT: Azpiroz, Ricardo
APPLICANT: Azpiroz, Ricardo
APPLICANT: Azpiroz, Sunghwa
APPLICANT: Feldmann, Kenneth A.
ITILE OF INVENTION: DWF4 POLYNUCLEOTIDES, POLYPEPTIDES AND USES THEREOF
ITILE OF INVENTION: DWF4 POLYNUCLEOTIDES, POLYPEPTIDES AND USES THEREOF
CURRENT APPLICATION NUMBER: US/10/804,772
CURRENT PILING DATE: 2000-02-11
FRIOR PILING DATE: 2000-02-11
PRIOR PILING DATE: 1999-02-11
PRIOR APPLICATION NUMBER: US 60/119,658
PRIOR PILING DATE: 1999-02-11
PRIOR PILING DATE: 1999-02-11
PRIOR PILING DATE: 1999-02-11
SPINOR FILING DATE: 1999-02-11
SPINOR FILING DATE: 1999-02-11
SPINOR PILING DATE: 1999-02-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 11;
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70.0%; Pred. No. 3.8e+02;
tive 3; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: 10
; OTHER INFORMATION: Xaa = Pro, Ala, or Val
US-10-804-772-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Xaa = Any Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Heme binding domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Exemplary sequence 1S-10-804-772-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 29, Application US/10804772 Publication No. US20040244077A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Xaa = Ala, Ser,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
Publication No. US20040244077A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 70.0
Matches 7; Conservative
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FGXGRRXCXG 11
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NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8th floor
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MEDIUM TYPE: Floppy disk
COMPUTER: INP PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 27-Feb-2003
CLASSIFICATION *CURROWN>
PRIOR APPLICATION *CURROWN>
PRIOR APPLICATION NUMBER: PCT/GB95/02465
FILING DATE: 18-OCT-1995
APPLICATION NUMBER: 09/970,751
FILING DATE: 17-MAR-1999
APPLICATION NUMBER: 08/945,161
FILING DATE: 17-APR-1999
APPLICATION NUMBER: 18-OCT-1995
APPLICATION NUMBER: 18-OCT-1999
APPLICATION NUMBER: 19-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 33; DB 4; Length 14; 100.0%; Pred. No. 4.7e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSE: NIXON & VANDERHYE P.C.
STREET: 1100 No. US20030198986A1th Glebe Rd.
CITY: Arlington
STATE: VA
      Score 33; DB 5;
Pred. No. 3.8e+02;
                                                  6; Mismatches
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MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-373-877-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAMB: Mitchard, Leonard C. REGISTRATION NUMBER: 29,009
                                                                                                                                                                                                                                                                                                                                    Rose, Kenneth A.
Stapleton, Genevieve
TITLE OF INVENTION: HIPPOCAMPUS
                                                                                                                                                                                                                         US-10-373-877-10
; Sequence 10, Application US/10373877
; Publication No. US20030198986A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 703-816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 703-816-4100 INFORMATION FOR SEQ ID NO: 10:
In 100.0%; Similarity 40.0%; 14; Conservative 6:
                                                                                                                                                                                                                                                                                                                APPLICANT: Lathe, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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Matches 10; Conserv
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APPLICANT: Lathe, Richard
Rose, Kenneth A.
Stapleton, Genevieve
Stapleton, Genevieve
TITLE OF INVENTION: HIPPOCAMPUS-ASSOCIATED PROTEINS; DNA
SEQUENCES CODING THEREFOR AND USED THEREOF
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 No. US20030198986A1th Glebe Rd. 8th floor
CITY: Arlington
                         8th floor
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                                                                                               Length 14;
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ZIP: 22201-474
ZIP: 22201-474
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM C compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 No. US20030198986A1th Glebe Rd.
CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 33; DB 4; L. Pred. No. 4.7e+02; 6; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Mitchard, Leonard C.
REGISTRATION NUMBER: 29,009
REFERENCE/DOCKET NUMBER: 604-572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 21, Application US/10373877; Publication No. US20030198986A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             n
Similarity 40.0%; 1
4; Conservative 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS:
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1 FGSGATICPG 10
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                                                                                      USA
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Best Local Similarity
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Publication No. US20030198986A1
GENERAL INFORMATION:
APPLICANT: Lathe, Richard
Rose, Kenneth A.
Stapleton, Genevieve
TITLE OF INVENTION: HIPPOCAMPUS-ASSOCIATED PROTEINS; DNA
SEQUENCES CODING THEREFOR AND USED THEREOF
                                                                                                              Rose, Kenneth A.
Stapleton, Genevieve
IIILE OF INVENTION: HIPPOCAMPUS-ASSOCIATED PROTEINS; DNA
SEQUENCES CODING THEREFOR AND USED THEREOF
                                                                                                                                                                                                                                                       8th floor
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COMPUTER: IMP PC compatible
COMPUTER: IMP PC compatible
COMPUTER: IMP PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/373,877
FILING DATE: 27-F6-2003
CIASSIFICATION NUMBER: PCT/GB95/02465
FILING DATE: 18-6CT-1995
APPLICATION NUMBER: 09/270,751
FILING DATE: 17-MAR-1999
APPLICATION NUMBER: 08/845,161
FILING DATE: 21-APR-1997
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: GB 9421093.7
FILING DATE: 21-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 33; DB 4; Length 14; 40.0%; Pred. No. 4.7e+02; tive 6; Mismatches 0; Indels
                                                                                                                                                                                                                                ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 No. US20030198986A1th Glebe Rd.
CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Mitchard, Leonard C.
REGISTRATION NUMBER: 29,009
REFERENCE/DOCKET NUMBER: 604-572
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
                           Sequence 19, Application US/10373877
Publication No. US20030198986A1
GENERAL INFORMATION:
APPLICANT: Lathe, Richard
                                                                                                                                                                                                                                                                                                                                      ZIP: 22201-4741
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 19
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                              NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
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1 FGLGTSKCPG 10
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Best Local Similarity
Matches 4; Conserve
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US-10-373-877-20
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            US-10-373-877-19
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Stapleton, Genevieve
TITLE OF INVENTION: HIPPOCAMPUS-ASSOCIATED PROTEINS; DNA
SEQUENCES CODING THEREFOR AND USED THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYBE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 No. US20030198986A1th Glebe Rd.
                                                                                                                                                                                                                                                                                                                                                                                                                                Score 33; DB 4;
Pred. No. 4.7e+02;
6; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/GB95/02465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/10/373,877
PILING DATE: 27-Feb-2003
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
                                                                 NAME: Mitchard, Leonard C.
REGISTRATION NUMBER: 29,009
REFERENCE/DOCKET NUMBER: 604-572
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
INFORMATION FOR SEQ ID NO: 22:
         APPLICATION NUMBER: GB 9421093.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 21-APR-1997
APPLICATION NUMBER: GB 9421093.7
FILING DATE: 19-OCT-1994
                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 18-OCT-1995
APPLICATION WUMBER: 09/270,751
ELING DATE: 17-MAR-1999
APPLICATION NUMBER: 08/845,161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Mitchard, Leonard C. REGISTRATION NUMBER: 29,009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 23, Application US/10373877
Publication No. US20030198986A1
GENERAL INFORMATION:
APPLICANT: Lathe, Richard
Rose, Kenneth A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                              STRANDEDNESS: <Unknown;
                                                                                                                                                                                                                                                  LENGTH: 14 amino acids
                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 FXXGXXXCXG 10
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PGFGMRQCLG 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR
                                                                                                                                                                                                                                                                                                                                                                                  US-10-373-877-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: HIPPOCAMPUS-ASSOCIATED PROTEINS; DN SEQUENCES CODING THEREFOR AND USED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 33; DB 4; Length 14; 40.0%; Pred. No. 4.7e+02; tive 6; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DAIA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSE: NIXON & VANDERHYE P.C.
STREET: 1100 No. US20030198986A1th Glebe Rd.
                                                                            PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB95/02465
FILING DATE: 18-0CT-1995
APPLICATION NUMBER: 09/270, 751
FILING DATE: 17-MAR-1999
APPLICATION NUMBER: 08/45,161
FILING DATE: 21-APR-1997
APPLICATION NUMBER: GB 9421093.7
FILING DATE: 19-0CT-1994
ATTORNEY/AGENT INFORMATION:

NAME: Mitchard, Leonard C.

REGISTRATION NUMBER: 29,009
REFERENCE/DOCKET NUMBER: 29,009
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/02465
FILING DATE: 18-OCT-1995
APPLICATION NUMBER: 09/270,751
                       : US/10/373,877
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FILING DATE: 27-Feb-2003
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-10-373-877-21
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APPLICATION NUMBER: 08/845,161
FILING DATE: 21-APR-1997
                                         FILING DATE: 27-Feb-2003
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 22, Application US/10373877
Publication No. US20030198986A1
GENERAL INFORMATION:
APPLICANT: Lathe, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 22201-4741
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 703-816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 14 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 703-816-4100
CURRENT APPLICATION DATA:
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SEQUENCE CHARACTERISTICS
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Best Local Similarity 40.0
Matches 4; Conservative
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1 FGAGPRSCVG 10
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8th floor

8th floor

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Stapleton, Genevieve
TITLE OF INVENTION: HIPPOCAMPUS-ASSOCIATED PROTEINS; DNA
SEQUENCES CODING THEREFOR AND USED THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/373,877
FILING DATE: 27-Feb-2003
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSE: NIVON & VANDERHYE P.C.
STREET: 1100 No. US20030198986Alth Glebe Rd.
CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 33; DB 4;
Pred. No. 4.7e+02;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/GB95/02465
FILING DATE: 18-OCT-1995
APPLICATION NUMBER: 09/270,751
FILING DATE: 17-MAR-1999
APPLICATION NUMBER: 08/845,161
FILING DATE: 21-APR-1997
FILING DATE: 19-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Mitchard, Leonard C.
REGISTRATION NUMBER: 29,009
REFERENCE/DOCKET NUMBER: 604-572
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-10-373-877-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 774, Application US/10865478; Publication No. US20040235041A1; GENERAL INFORMATION:
                                                                                                                             RESULT 21
US-10-373-877-25
US-10-373-877-25
Sequence 25, Application US/10373877
Publication No. US20030198986A1
GENERAL INFORMATION:
APPLICANT: Lathe, Richard
ROSS, Kenneth A.
ROSS, Kenneth A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 22201-4741
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 703-816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELEFAX: 703-816-4100
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40.0%; E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
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Best Local Similarity 40.0
Matches 4; Conservative
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1 FGYGVRACLG 10
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1 FGWGVRQCLG 10
             FXXGXXXCXG 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stapleton, Genevieve
TITLE OF INVENTION: HIPPOCAMPUS-ASSOCIATED PROTEINS; DNA
SEQUENCES CODING THEREFOR AND USED THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 No. US20030198986A1th Glebe Rd. 8th floor
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC COMPATIBLE

COMPUTER: BATCHORY

OPERATING SYSTEM: PC-DOS/MS-DOS

COPERATING SYSTEM: PC-DOS/MS-DOS

COPTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/373,877

FILING DATE: 12-RP-2003

CLASSIFICATION NUMBER: PCT/GB95/02465

FILING DATE: 18-OCT-1995

APPLICATION NUMBER: 09/270,751

FILING DATE: 17-MAR-1999

APPLICATION NUMBER: GB 9421093.7

FILING DATE: 21-APR-1997

ATTORNEY/AGENT NUMBER: GB 9421093.7

FILING DATE: 30-OCT-1994

ATTORNEY/AGENT NUMBER: 100-OCT-1994
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                                                                                                                                                                     100.0%; Score 33; DB 4; Length 14; 40.0%; Pred. No. 4.7e+02; tive 6; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Mitchard, Leonard C.
REGISTRATION NUMBER: 29,009
REFERENCE/DOCKET NUMBER: 604-572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-10-373-877-24
                                                   TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-10-373-877-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
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Publication No. US20030198986A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: <Unknown>
                  TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lathe, Richard
Rose, Kenneth A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 703-816-4100 INFORMATION FOR SEQ ID NO: 24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 45
                                                                                                                                                                     Query Match
Best Local Similarity 40.0
Matches 4; Conservative
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1 FGCGARVCLG 10
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Best Local Similarity
Matches 4, Conserva
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Gaps

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Length 14; Indels

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APPLICANT: Ranshaw, Heather A.

TITLE OF INVENTION: A Thymus Expressed Human Cytochrome P450 (P450TEC)

TITLE OF INVENTION: A Thymus Expressed Human Cytochrome P450 (P450TEC)

FILE REFERENCE: 11812-65

CURRENT APPLICATION NUMBER: US/10/257,378

CURRENT FILING DATE: 2000-06-01

PRIOR FILING DATE: 2000-06-01

PRIOR FILING DATE: 2000-04-20

NUMBER OF SEQ ID NOS: 56

SOFTWARE: Patentin Ver. 2.1

LENGTH: 15

TYPE: TTYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: query sequence
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OTHER INFORMATION: Xaa can be any amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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INFORMATION: Xaa can be amino acid
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THER INFORMATION: Xaa can be Gly or Ser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: (14)
; OTHER INFORMATION: Xaa can be Phe, Leu,
US-10-257-378-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       can be any amino
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 17, Application US/10882241
Publication No. US20050114910A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 10; Conservative
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OTHER INFORMATION: Xaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Xaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: LONE, YU-CHUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: UNSURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IAME/KEY: UNSURE
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                                                                                       APPLICANT: Shimkets, Richard A.
APPLICANT: Leach, Martin D.
TITLE OF INVENTION: Gâingle Nucleotide Polymorphisms for Known Genes FILE REPERSHOE: 15966-534-CIP1
CURRENT APPLICATION NUMBER: US/10/865,478
CURRENT FILING DATE: 2004-0-4-1
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TITLE OF INVENTION: Methods for Expressing Gene Products;
FILLE REPERENCE: 183996/2002;
CURRENT APPLICATION NUMBER: US/09/957,674
CURRENT FILING DATE: 2001-09-20;
PRIOR APPLICATION NUMBER: GB990736;
PRIOR PILING DATE: 1999-03-30;
PRIOR PILING DATE: 1999-03-30;
PRIOR FILING DATE: 2000-03-30;
NUMBER OF SEQ ID NOS: 16;
SOFTWARE: PATENTIN VETSION 3.1;
SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 3; Length 15;
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                                                                                                                                                                                                           CURRENT FILING DATE: 2004-06-10
PRIOR APPLICATION NUMBER: 60/109,024
PRIOR FILING DATE: 1998-11-17
PRIOR FILING DATE: 1999-11-16
PRIOR FILING DATE: 1999-11-16
PRIOR FILING DATE: 1999-11-16
PRIOR FILING DATE: 1999-11-16
PRIOR PILING DATE: 1999-11-16
PRIOR PILING DATE: 1999-11-16
PRIOR PILING DATE: 1999-11-17
NUMBER OF SEQ ID NOS: 880
SOFTWARE: Curaden Patent Formatter Version 0.9
SEQ ID NO 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (7)...(0)
OTHER INFORMATION: cSNP translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 13, Application US/09957674 Patent No. US20020120948A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/10257378
Publication No. US20030190642A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Petkovich, P. Martin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40.04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Hepatitis B virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Jones, Glenville APPLICANT: Petkovich. P. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Conservative
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FHYGVLACEG 11
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FLGGITVCLG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 4; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 4; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-865-478-774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-957-674-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 24
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1 FXXGXXXCXG 10
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4 FFFGNSPCCG 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 02109-1875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION: -14..-1
US-10-926-683-1257
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: RELOCAS E. CARROLL
APPLICANT: Blace P. Heppard
APPLICANT: No. US20030126645Aluhiro Nagasawa
APPLICANT: No. US20030126645Aluhiro Nagasawa
APPLICANT: No. US20030126645Aluhiro Nagasawa
TITLE OF INVENTINE SHARTON Alteration Of Embryo/Endosperm Size During Seed Development
FILE REFERENCE: BB1487 US NA
FILE REFERENCE: BB1487 US NA
CURRENT APPLICATION NUMBER: 60/295,921
PRIOR APPLICATION NUMBER: 60/295,921
PRIOR APPLICATION NUMBER: 60/395,921
PRIOR APPLICATION NUMBER: 60/334,317
PRIOR PLING DATE: 2001-11-28
NUMBER OF SEQ ID NOS: 111
SEQ ID NO 90
LENGTH: 16
    COMPLEX (MHC) PHENOTYPE, EXPERIMENTAL USES AND APPLICATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: Peptide
US-10-882-241-17
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                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 33; DB 5; Length 15; 40.0%; Pred. No. 5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    6; Mismatches
; TITLE OF INVENTION: COMPLEX (MHC) PHENOTYPE
FILE REFERENCE: 03495.0319
CURRENT APPLICATION NUMBER: US/10/882,241
FURRENT APPLICATION NUMBER: 60/490,945
PRIOR APPLICATION NUMBER: 60/490,945
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 3.2
; SOQ ID NO 17
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: (13)...(13); OTHER INFORMATION: Xaa = any amino acid US-10-163-198-90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (9)..(9)
OTHER INFORMATION: Xaa = any amino acid
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Publication No. US20050106595A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 26
US-10-163-198-90
; Sequence 90, Application US/10163198
; Publication No. US20030126645A1
; GENERAL INFORMATION:
; APPLICANT: Rebecca E. Cahoon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: conserved sequence motif
                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 40.0
Matches 4; Conservative
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7 FGXGRRXCPG 16
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5 FLGGTTVCLG 14
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Best Local Similarity
Matches 6; Conservi
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US-10-926-683-1257
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APPLICANT: Duclert A.
APPLICANT: Duclert A.
APPLICANT: Duclert A.
APPLICANT: Duclert A.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: GENSET. 025CP1
CURRENT FILING DATE: 2004-08-25
CURRENT FILING DATE: 1999-12-21
PRIOR PLING DATE: 1999-12-21
PRIOR PLING DATE: 1999-12-21
PRIOR PLING DATE: 1999-10-09
PRIOR PELING DATE: 1998-04-09
PRIOR PLING DATE: 1998-04-09
PRIOR PLING DATE: 1998-04-09
PRIOR PLING DATE: 1998-04-09
NUMBER OF SEQ ID NOS: 1622
SOFTWARE: Patent.pm
: SEQ ID NO 1257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Seidman, Christine
APPLICANT: Seidman, Jonathan
APPLICANT: Thierfelder, Ludwig
APPLICANT: Thierfelder, Ludwig
APPLICANT: Watkins, Hugh
APPLICANT: Mare Calum
TITLE OF INVENTION: With Hypertrophic Cardiomyopathy
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: BOSTON
STREET: MASSACHUSELTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 33; DB 5; Length 16;
Pred. No. 5.3e+02;
6; Mismatches 0; Indels
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COMPUTER: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NDATA:
APPLICATION NUMBER: US/08/647,444
FILING DATE: 11-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12, Application US/08647444 Publication No. US20020127548A1 GENERAL INFORMATION:
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NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFRENCE/DOCKET NUMBER: IGI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.08;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage COMPUTER: COMPAQ, IBM PC compatible OPERATING SYSTEM, MS-DOS 5.1
SOFTWARE: WORD PERFECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/855,595
FILING DATE: 28-May-2004
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 20;
                                                                                                                                                                     APPLICANT: Perkovich, P. Martin, White, Jay A.,
Beckett, Barbara R., Jones, Glenville
TITLE OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Petkovich, P. Martin, White, Jay A., Beckett, Barbara R., Jones, Glenville ITLE OF INVENTION: Retinoid Metabolizing Protein NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS: ADDRESSE: Blake, Cassels & Graydon STREET: Box 25, Commerce Court West
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 33; DB 5; 40.0%; Pred. No. 6.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 36,424
REFERENCE/DOCKET NUMBER: 50767/00010
                                                                                                                                                                                                                                                                                      ADDRESSEE: Blake, Cassels & Graydon
STREET: Box 25, Commerce Court West
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/668,482
FILING DATE: 25-Sep-2000
APPLICATION NUMBER: 08/882,164
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5; Mismatches
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APPLICATION NUMBER: 08/667, 546
FILING DATE: June 21, 1996
APPLICATION NUMBER: 08/724,466
FILING DATE: OCCODER: 1, 1996
ATTORNEY/AGENT INFORMATION:
NAME: HULL, JOHN C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                           RESULT 30
US-10-855-595-7
Sequence 7, Application US/10855595
Publication No. US20040235057A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/10855595 Publication No. US20040235057A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40.0%;
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Best Local Similarity 40.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                      STATE: Ontario
COUNTRY: Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 FXXGXXXCXG 10
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2 FSGGARNCIG 11
  2 FGGGPRLCPG 11
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US-10-855-595-8
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                                                                                                                                                                                              DB 2; Length 18; 5.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.4 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/10855595
Publication No. US20040235057A1
GENERAL INFORMATION:
APPLICANT: Perkovich, P. Martin, White, Jay A.,
BECKEL, Barbara R., Jones, Glenville
TITLE OF INVENTION: Retinoid Metabolizing Protein
NUMBER OF SEQUENCES: 43
CORRESONDENCE ADDRESS:
ADDRESSEE: Blake, Cassels & Graydon
STREET: Box 25, Commerce Court West
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 36,424
REFERENCE/DOCKET NUMBER: 50767/00010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/668,482
FILING DATE: 25-Sep-2000
APPLICATION NUMBER: 08/882,164
FILING DATE: June 25, 1997
APPLICATION NUMBER: 08/67,546
FILING DATE: June 21, 1996
APPLICATION NUMBER: 08/124,466
FILING DATE: October 1, 1996
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPEs Diskette, 3 1/2 inch, 1
COMPUTER: COMPAQ, IBM PC compatible
OPERATING SYSTEM: MS-DOS 5.1
                                                                                                                                                                                                                   Pred. No. 5.96
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/10/855,595
FILING DATE: 28-May-2004
PRIOR APPLICATION DATA:
                                                                                                                                                                                              Score 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE DESCRIPTION: SEQ ID NO: 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
                                                                                                                                                                                              100.08;
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                     40.04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (416)
                                         SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                            Query Match 100.
Best Local Similarity 40.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Ontario
COUNTRY: Canada
ZIP: MSL 1A9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 40.0
Matches 4; Conservative
                                                                                                                     , MOLECULE TYPE: protein US-08-647-444-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION
                                                                                                                                                                                                                                                                                        1 FXXGXXXCXG 10
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FDGGIYVCGG 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 FXXGXXXCXG 10
                                                                                  TYPE: amino acid
TOPOLOGY: linear
                    INFORMATION FOR
                                                                                                                                                                                                                                                                                                                                                                                             RESULT 29
US-10-855-595-6
TELEPAX:
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Gaps

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APPLICATION NUMBER: US/10/855,595
FILING DATE: 28-May-2004
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 33; DB 5; Length 20;
Pred. No. 6.6e+02;
6; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10, Application US/1085595
Publication No. US20040235057A1
GENERAL INFORMATION:
APPLICANT: Perkovich, P. Martin, White, Jay A.,
APPLICANT: Perkovich, P. Martin, White, Jay A.,
Beckett, Barbara R., Jones, Glenville
TITLE OF INFORTION: Retinoid Metabolizing Protein
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
                                                                                                                                       NAME: Hunt, John C.
REGISTRATION NUMBER: 36,424
REGISTRATION NUMBER: 50767/00010
TELECOMMUNICATION INFORMATION:
TELEFAX: (416) 863-4344
TELEFAX: (416) 863-2653
INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 36,424
REFERENCE/DOCKET NUMBER: 50767/00010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/668,482
FILING DATE: 25-590-2000
FILING DATE: 05-590-2000
FILING DATE: June 25, 1997
APPLICATION NUMBER: 08/67,546
APPLICATION NUMBER: 08/67,466
APPLICATION NUMBER: 08/724,466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Blake, Cassels & Graydon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: Box 25, Commerce Court West CITY: Toronto
FILING DATE: June 25, 1997
APPLICATION NUMBER: 08/667,546
FILING DATE: June 21, 1996
APPLICATION NUMBER: 08/724,466
FILING DATE: October 1, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: October 1, 1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO:
US-10-855-595-9
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TELEPHONE: (416) 863-4344
                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Ontario
COUNTRY: Canada
ZIP: M5L 1A9
COMPUTER READABLE FORM:
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Best Local Similarity 40.0
Matches 4; Conservative
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2 FGTGPRNCIG 11
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ZIP: M5L 1A9
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
COMPUTER: COMPAO, IBM PC compatible
OPERATING SYSTEM: MS-DOS 5.1
SOFTWARE: WORD PERFECT
                                                                                               MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage COMPUTER: COMPAQ, IBM PC compatible OPERATING SYSTEM MS-DOS 5.1 SOFTWARE: WORD PERFECT CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 33; DB 5; Length 20;
40.0%; Pred. No. 6.6e+02;
tive 6; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9, Application US/1085595

Publication No. US20040235057A1

GENERAL INFORMATION:

APPLICANT: Peckovich, P. Martin, White, Jay A.,

ITLE OF INVENTION: Retinoid Metabolizing Protein

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

ADDRESSEE: Blake, Cassels & Graydon

STREET: Box 25, Commerce Court West

CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Hunt, John C.
REGISTRATION NUMBER: 36,424
REFERENCE/FOCKET NUMBER: 50767/00010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 863-4344
TELEFAX: (416) 863-2653
                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/668,482
FILING DATE: 25-Sep-2000
APPLICATION NUMBER: 08/682,164
FILING DATE: June 25, 1997
APPLICATION NUMBER: 08/667,546
FILING DATE: June 21, 1996
APPLICATION NUMBER: 08/724,466
FILING DATE: October 1, 1996
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APPLICATION NUMBER: US/10/855,595
FILING DATE: 28-May-2004
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/668,482
FILING DATE: 25-Sep-2000
                                                                                                                                                                                                                       APPLICATION NUMBER: US/10/855,595
FILING DATE: 28-May-2004
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE DESCRIPTION: SEQ ID NO: 8 US-10-855-595-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
     STATE: Ontario
COUNTRY: Canada
ZIP: M5L 1A9
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 4; Conserva
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ZIP: M5L 1A9
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
COMPUTER: COMPAQ, IBM PC compatible
OPERATING SYSTEM: MS-DOS 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 20;
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Publication No. US20040259074A1
GENERAL INFORMATION:
    APPLICANT: Petkovich, P. Martin, White, Jay A.,
    Beckett, Barbara R., Jones, Glenville
    TITLE OF INVENTION: Retinoid Metabolizing Protein
    NUMBER OF SEQUENCES: 43
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Blake, Cassels & Graydon
    STREET: Box 25, Commerce Court West
                                                                                                                                                                          Beckett, Barbara R., Jones, Glenville TITLE OF INVENTION: Retinoid Metabolizing Protein
                                                      3-10-855-532-7
Sequence 7, Application US/1085532
Publication No. US20040259074A1
GENERAL INFORMATION:
APPLICANT: Petkovich, P. Martin, White, Jay A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 33; DB 5;
40.0%; Pred. No. 6.6e+02;
trive 6; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 36,424
REPERENCE/DOCKET NUMBER: 50767/00010
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Blake, Cassels & Graydon
STREET: Box 25, Commerce Court West
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/668,482
FILING DATE: 25-Sep-2000
PPLICATION NUMBER: 08/882,164
FILING DATE: June 25, 1997
APPLICATION NUMBER: 08/667,546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: WORD PERFECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/855,532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: June 21, 1996
APPLICATION WUNBER: 08/724,466
FILING DATE: October 1, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear ; SEQUENCE DESCRIPTION: SEQ ID NO: US-10-855-532-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (416) 863-4344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PILING DATE: 28-May-2004
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (416) 863-2653
INFORMATION FOR SEQ ID NO: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 40.0
Best Local 4; Conservative
                                                                                                                                                                                                                                                                                                                                               STATE: Ontario
COUNTRY: Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Ontario
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                         RESULT 35
US-10-855-532-7
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                                                                                                                                                                          Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Petkovich, P. Martin, White, Jay A., Beckett, Barbara R., Jones, Glenville BITLE OF INVENTION: Retinoid Metabolizing Protein NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS: ADDRESSE: Blake, Cassels & Graydon
                                                                                                                                                                       Query Match 100.0%; Score 33; DB 5; Best Local Similarity 40.0%; Pred. No. 6.6e+02; Matches 4; Conservative 6; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 50767/00010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/668,482
FILING DATE: 25-Sep-2000
APPLICATION NUMBER: 08/682,164
FILING DATE: June 25, 1997
APPLICATION NUMBER: 08/667,546
FILING DATE: June 21, 1996
APPLICATION NUMBER: 08/724,466
FILING DATE: October 1, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Blake, Cassels & Graydon STREET: Box 25, Commerce Court West
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Disekette, 3 1/2 inch,
COMPUTER: COMPAQ, IBW PC compatibl
OPERATING SYSTEM: MS-DOS 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/10/855,532 FILING DATE: 28-May-2004 PRIOR APPLICATION DATA:
TYPE: amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 10
US-10-855-595-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE DESCRIPTION: SEQ ID NO: 6
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TELEFAX: (416) 863-2653
INFORMATION FOR SEQ ID NO: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/10855532
Publication No. US20040259074A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: WORD PERFECT CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
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COUNTRY: Canada
ZIP: M5L 1A9
                                                                                                                                                                                                                                                                      PXXGXXXCXG 10
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FSGGSRNCIG 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-855-532-6
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CITY: TOCOLO
CITY: TOCOLO
COUNTRY: Canada
COUNTRY: Canada
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
COMPUTER: COMPA, IBM PC compatible
COMPUTER: COMPA, IBM PC compatible
COMPUTER: COMPA, IBM PC compatible
OPERATING SYSTEM: MS-DOS 5.1
SOFTWARE: WORD PERPECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/855,532
PRIOR APPLICATION NUMBER: US/09/668,482
PRICATION NUMBER: 08/82,164
PILING DATE: June 25, 1997
APPLICATION NUMBER: 08/862,164
FILING DATE: June 25, 1997
APPLICATION NUMBER: 08/67,546
FILING DATE: June 21, 1996
RELIGING DATE: October 1, 1996
RELIGING DATE: October 1, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 20;
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CORRESPONDENCE ADDRESS: ADDRESSE: Blake, Cassels & Graydon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 33; DB 5;
Pred. No. 6.6e+02;
6; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 36,424
REFERENCE/DOCKET NUMBER: 50767/00010
TELECOMMUNICATION INFORMATION:
                                                                                                                                                    NAME: Hunt, John C.
REGISTRATION NUMBER: 36,424
REGISTRATION NUMBER: 50767/00010
TELECOMUNICATION INFORMATION:
TELEPHONE: (416) 863-4344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: Box 25, Commerce Court
APPLICATION NUMBER: 08/667,546
FILING DATE: June 21, 1996
APPLICATION NUMBER: 08/724,466
FILING DATE: October 1, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence description: Seq ID NO: 9 US-10-855-532-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10, Application US/1085532
Publication No. US20040259074A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acids
STRANDEDNESS: single
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40.0%; F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPÓLOGY: linear
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Best Local Similarity 40.0
Matches 4; Conservative
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| Sequence 9, Application US/1085532
| Publication No. US20040259074A1
| Publication No. US20040259074A1
| GENERAL INFORMATION:
| APPLICANT: Petkovich, P. Martin, White, Jay A., Beckett, Barbara R., Jones, Glenville
| TITLE OF INVENTION: Retinoid Metabolizing Protein NUMBER OF SEQUENCES: 43
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Blake, Cassels & Graydon STREET: Blake, Cassels & Graydon STREET: Blake, Cassels & Graydon STRATE: Ontario
| CITY: Toronto STRATE: Ontario
| COUNTRY: Canada ZIP: MSL 1A9
| COMPUTER READABLE FORM: MSDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage COMPUTER: COMPAC, IBM PC Compatible OPERATING SYSTEM: MS-DOS 5.1
| SOFTWARE: WORD PERFECT CURRENT APPLICATION DATA: ADDITATION WILLIAM NATION NATA: ADDITATION WILLIAM NATALINE COMPACE NATION NATA: ADDITATION WILLIAM NATALINE NAT
                                     ZIP: M5L 1A9
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage COMPUTER: COMPAQ, IBM PC compatible OPERATING SYSTEM: MS-DOS 5.1
SOFTWARE: WORD PERFECT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 33; DB 5; Length 20; 40.0%; Pred. No. 6.6e+02; tive 6; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 36,424
REFERENCE/DOCKET NUMBER: 50767/00010
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                          CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/655,532
FILING DATE: 28-May-2004
PRIOR APPLICATION NUMBER: US/09/668,482
FILING DATE: 25-Sep-2000
APPLICATION NUMBER: 08/682,164
FILING DATE: JE-Sep-2000
APPLICATION NUMBER: 08/67,546
FILING DATE: June 25, 1997
APPLICATION NUMBER: 08/67,546
FILING DATE: OCTOBER: 1, 1996
APPLICATION NUMBER: 08/724,466
FILING DATE: OCTOBER: 1, 1996
ATTORNEY AGENT INFORMATION:
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FILING DATE: 25-569-200
APPLICATION NUMBER: 08/882,164
FILING DATE: June 25, 1997
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SEQUENCE DESCRIPTION: SEQ ID NO: 8
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TELEFAX: (416) 863-2653
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 40.0°
          COUNTRY: Canada
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FSGGARNCIG 11
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Pred. No. 7.5e+02;
6; Mismatches 0; Indels
                                                                                                                                                                   Length 21
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FILE REFERENCE: 2314-227
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                                                                                                                                                                   Score 33; DB 5;
Pred. No. 6.9e+02;
                                              ; TYPE: PRT
; ORGANISM: aspergillus ochraceus 11aOH peptide 3
US-10-900-856-28
                                                                                                                                                                                          Pred. No. 6.966; Mismatches
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Patent No. US20020173449A1
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McIntosh, J. Michael
Layer, Richard T.
Jones, Robert M.
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Cartier, G. Edward
Watkins, Maren
                                                                                                                                                                   100.0%;
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40.0%;
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Best Local Similarity 40.0
Matches 4; Conservative
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4 FGHGVHACPG 13
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5 FLLGFLGCCG 14
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ORGANISM: Homo sapiens
                                                                                                                                                                                     Best_Local_Similarity
Matches 4; Conserv
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  SEQ ID NO 28
LENGTH: 21
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APPLICANT: Lealie, Engel C
APPLICANT: Lealie, Engel C
APPLICANT: Dean, Messing M
APPLICANT: Dean, Messing M
APPLICANT: Beverly, Reitz A
APPLICANT: Scott, Vaccaro A
APPLICANT: Scott, Vaccaro A
APPLICANT: Ping, Wang T
APPLICANT: Robin, Weinberg A
APPLICANT: Robin Weinberg A
APPLICANT: We
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                                                                                                                                 h Similarity 40.0%; Score 33; DB 5; Length 20; Similarity 40.0%; Pred. No. 6.6e+02; 4; Conservative 6; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Robin A. Weinberg
TITLE OF INVENTION: Aspergillus ochraceus 11 alpha
TITLE OF INVENTION: hydroxylase and oxidoreductase
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CURRENT APPLICATION NUMBER: US/10/021,425
CURRENT FILING DATE: 2001-10-30
                            TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 10
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STRANDEDNESS: single
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Mark C. Walker
Ping T. Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alan M. Easton
Leslie C. Engel
Dean M. Messing
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FSGGSRNCIG 11
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FGHGVHACPG 13
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Best Local Similarity
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Best Local Similarity
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                                                                             US-10-855-532-10
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LENGTH: 21
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                                                                                                                                                                                          Matches
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Gaps

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; LOCATION: (1)..(30)
; OTHER INFORMATION: Xaa at residues 3and 5 may be Glu or gamma-carboxy-Glu; Xaa at re; OTHER INFORMATION: Sidues 6, 7, 18 and 19 may be Pro or hydroxy-Pro; Xaa at residues ; OTHER INFORMATION: 24 and 28 may be Trp or bromo-Trp
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Publication No. US20040131617A1
GENERAL INFORMATION:
APPLICANT: WHITE, Jay A.
APPLICANT: WHITE, Jay A.
APPLICANT: PETKOVICH, P. Martin
APPLICANT: TONES, Glenville
APPLICANT: RAMSHW, Heather
TITLE OF INVENTION: P450RA1-2 (P450 Cytochrome 26B), Encoding Nucleic Acid
TITLE OF INVENTION: Molecules and Methods and Uses Thereof
FILE REPERENCE: 11812-78
CURRENT APPLICATION NUMBER: US/10/433,485A
CURRENT APPLICATION NUMBER: PCT/CA01/01805
PRIOR PILING DATE: 2001-12-17
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Pred. No. 9.5e+02;
4; Mismatches 0; IndelB
                                Indels
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APPLICANT: Cogneta, Baldomero M.
APPLICANT: Cartier, G. Edward
APPLICANT: Watkins, Maren
APPLICANT: Watkins, Maren
APPLICANT: Watkins, Maren
APPLICANT: McIntosh, J. Michael
APPLICANT: Layer, Richard T.
APPLICANT: Layer, Richard T.
APPLICANT: Jones, Pobert M.
TITLE OF INVENTION: O-Superfamily Conotoxin Peptides
FILE REFERENCE: 2314-227
CURRENT FILING DATE: 2000-12-28
FRIOR APPLICATION NUMBER: US 60/243,412
PRIOR APPLICATION NUMBER: US 60/214,263
PRIOR APPLICATION NUMBER: US 60/214,263
PRIOR APPLICATION NUMBER: US 60/214,263
PRIOR PILING DATE: 2000-00-20
PRIOR PELING DATE: 2000-00-20
PRIOR APPLICATION NUMBER: US 60/214,263
PRIOR FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 409
SEQ ID NO SEQ ID NOS: 409
SEQ ID NO 283
LENGTH: 30
Pred. No. 9.5e+02;
4; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: University of Utah Research Foundation APPLICANT: Cognetix, Inc.
                                                                                                                                                                                                                                                                                           Sequence 283, Application US/09749637A Patent No. US20020173449A1 GENERAL INFORMATION:
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100.0%;
Best Local Similarity 60.0%;
Matches 6; Conservative 4
     60.08;
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ORGANISM: Conus geographus
  Best Local Similarity 60.0
Matches 6; Conservative
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14 FKIGXXCCSG 23
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14 FKIGXXCCSG 23
                                                                                         1 PXXCXXXCXG
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LOCATION: (1)..(30)

OTHER INFORMATION: Xaa at residues 3 and 5 may be Glu or gamma-carboxy-Glu; Xaa at x
OTHER INFORMATION: esidues 6, 7, 18 and 19 may be Pro or hydroxy-Pro; Xaa at residue
OTHER INFORMATION: s 24 and 28 may be Trp or bromo-Trp
US-09-749-637A-129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (1)...(30)
OTHER INFORMATION: esidues 6, 7, 18 and 19 may be Glu or gamma-carboxy-Glu; Kaa at residue
OTHER INFORMATION: esidues 6, 7, 18 and 19 may be Pro or hydroxy-Pro; Kaa at residue
OTHER INFORMATION: 8 24 and 28 may be Trp or bromo-Trp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 33; DB 3; Length 30; 60.0%; Pred. No. 9.5e+02; tive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GRNEALL INFORMATION:
GRNEALL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: Cattier, G. Edward
APPLICANT: Gartier, G. Edward
APPLICANT: Gartier, G. Edward
APPLICANT: Hillyard, David R.
APPLICANT: Hillyard, David R.
APPLICANT: McIncosh, J. Michael
APPLICANT: Jones, Robert M.
APPLICANT: Jones, Robert M.
APPLICANT: Jones, Robert M.
FILE REFERENCE: 2314-227
CURRENT APPLICATION NUMBER: US/09/749,637A
CURRENT APPLICATION NUMBER: US 60/243,412
FRIOR FILING DATE: 2000-10-27
FRIOR FILING DATE: 2000-07-20
FRIOR FILING DATE: 2000-07-20
FRIOR FILING DATE: 2000-07-20
FRIOR FILING DATE: 2000-06-26
FRIOR FILING DATE: 2000-07-20
FRIOR FILING DATE: 2000-06-26
FRIOR FILING DATE: 2000-06-26
FRIOR FILING DATE: 2000-06-26
FRIOR FILING DATE: 2000-06-26
FRIOR FILING DATE: 1999-12-30
SOFTWARE PALCHIN VUMBER: US 60/173,754
FRIOR FILING DATE: 1999-12-30
SOFTWARE PALCHIN VUMBER: US 60/173,754
FRIOR FILING DATE: 1999-12-30
SEQ ID NO 129
CURRENT FILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: US 60/243,412
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-07-20
PRIOR FILING DATE: 2000-07-20
PRIOR PILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: US 60/214,263
PRIOR FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 409
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 129, Application US/09749637A Patent No. US20020173449A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Conus marmoreus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Conus striatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 FXXGXXXCXG 10
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14 FKIGXXCCSG 23
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Gaps

100.0%; Score 33; DB 3; Length 30;

Query Match

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LOCATION: (1)..(30)
OTHER INFORMATION: Saa at residues 3 and 5 may be Glu or gamma-carboxy-Glu; Xaa at r
OTHER INFORMATION: esidues 6, 7, 18 and 19 may be Pro or hydroxy-Pro; Xaa at residue
OTHER INFORMATION: s 24 and 28 may be Trp or bromo-Trp
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                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Hillyard, David R.
APPLICANT: McIntosh, J. Michael
APPLICANT: Layer, Richard T.
APPLICANT: Jones, Robert M.
TITLE OF INVENTION: O-Superfamily Conotoxin Peptides
FILE REFERENCE: 2314-277
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APPLICANT: McIntosh, J. Michael
APPLICANT: Layer, Richard T.
APPLICANT: Jones, Robert M.
TITLE OF INVENTION: O-Superfamily Conotoxin Peptides
FILE REFERENCE: 2314-277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 33; DB 5; L
Pred. No. 9.5e+02;
4; Mismatches 0;
                                                                                                                                                                                 Publication No. 2007.

APPLICANT: University of Utah Research Foundation APPLICANT: University of Utah Research Foundation APPLICANT: Cognetix, Inc. APPLICANT: Olivera, Baldomero M. APPLICANT: Cartier, G. Edward APPLICANT: Watkins, Maren
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APPLICANT: Oliveza, Baldomero M.
APPLICANT: Cartier, G. Edward
APPLICANT: Watkins, Maren
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CURRENT PEDLICATION NUMBER: US/10/839,227
CURRENT FILING DATE: 2004-05-06
PRIOR APPLICATION NUMBER: US 09/749,637
PRIOR PILING DATE: 2000-12-28
PRIOR PRIOR APPLICATION NUMBER: US 60/243,412
PRIOR FILING DATE: 2000-0-27
PRIOR FILING DATE: 2000-07-20
PRIOR FILING DATE: 2000-07-20
PRIOR FILING DATE: 2000-06-26
PRIOR FILING DATE: 1999-12-30
PRIOR FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 409
SOFTWARER: PARCHIN VERSION 3:0
SOFTWARER: PARCHIN VERSION 3:0
SOFTWARER: 98 ARCHIN VERSION 3:0
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CURRENT FILING DATE: 2004-05-06
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                                                                                                                                              Sequence 129, Application US/10839227
Publication No. US20050214903A1
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60.0%; P
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ORGANISM: Conus striatus
FEATURE:
NAME/KSY: SITE
LOCATION: (1)..(30)
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Matches 6; Conservative
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14 PKIGXXCCSG 23
        14 FKIGXXCCSG 23
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CTHER INFORMATION: Xaa at residues 3 and 5 may be Glu or gamma-carboxy-Glu; Xaa at r other Information: esidues 6, 7, 18 and 19 may be Pro or hydroxy-Pro; Xaa at residue; OTHER INFORMATION: s 24 and 28 may be Trp or bromo-Trp
                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: typical heme binding motif found in all Cytochrome P4508 US-10-433-485A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
100.0%; Score 33; DB 4; Length 30;
Best Local Similarity 40.0%; Pred. No. 9.5e+02;
Matches 4; Conservative 6; Mismatches 0; Indels
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APPLICANT: Cornetix, Inc.
APPLICANT: Cornetix, Inc.
APPLICANT: Cornetix, Inc.
APPLICANT: Cartier, G. Edward
APPLICANT: Cartier, G. Edward
APPLICANT: Hillyard, David R.
APPLICANT: McIntosh, J. Michael
APPLICANT: McIntosh, J. Michael
APPLICANT: McIntosh, J. Michael
APPLICANT: Jones, Robert M.
TITLE OF INVENTION: O-Superfamily Conotoxin Peptides
FILE REFERENCE: 2314-277
CURRENT FILING DATE: 2004-05-06
PRIOR PILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: US 60/243,412
PRIOR APPLICATION NUMBER: US 60/219,440
PRIOR PILING DATE: 2000-07-20
PRIOR PILING DATE: 2000-07-20
PRIOR PILING DATE: 2000-07-20
PRIOR FILING DATE: 2000-06-26
PRIOR FILING DATE: 2000-06-26
PRIOR FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 409
SOFTWARE: Patentin version 3.0
SEQ ID NO 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: University of Utah Research Foundation
PRIOR APPLICATION NUMBER: PCT/CA00/01493
PRIOR FILING DATE: 2000-12-15
PRIOR PILING DATE: 2000-01-27
PRIOR PILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: 60/171,110
PRIOR APPLICATION NUMBER: 60/171,110
NUMBER OF SEQ ID NOS: 48
SOFWARE: Patentin version 3.0
LENGTH: 30
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Publication No. US20050214903A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
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8 FGIGKRVCMG 17
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Gaps

CURRENT FILING DATE: 2004-05-06 PRIOR APPLICATION NUMBER: US 09/749,637

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APPLICANT: ALMORT, M.
APPLICANT: ALMORT, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: HYBRID POLYPEPTIDES
FILE REFERENCE: 7822-100
CURRENT FILING DATE: 2003-01-24
PRIOR PLICATION NUMBER: 09/350,641
PRIOR PAPLICATION NUMBER: 09/350,641
PRIOR PLILING DATE: 1999-05-20
PRIOR FILING DATE: 1999-05-20
PRIOR FILING DATE: 1999-05-20
PRIOR FILING DATE: 1998-05-20
SOFTWARE: PASEC for Windows Version 3.0
SEQ ID NO 487
LENGTH: 35
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Pred. No. 1.1e+03;
6; Mismatches 0; Indels
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Job time : 167 sec8
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Best Local Similarity 40.0%; Matches 4; Conservative 6
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26 FLGGTTVCLG 35
                            Guthrie, K.
Merutka, G.
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; Sequence 159510, Application US/10437963
; Publication No. US2004012334341
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Zhou, Yongwei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Bukharov, Andrey A.
; APPLICANT: Bradalk, Brad
; APPLICANT: Bradalk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION NUMBER: US/10/437,963
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT PILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 159510
                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:

NAME/KEX: SITE

LOCATION: (1)..(30)

OTHER INFORMATION: Xaa at residues 3and 5 may be Glu or gamma-carboxy-Glu; Xaa at re
OTHER INFORMATION: sidues 6, 7, 18 and 19 may be Pro or hydroxy-Pro; Xaa at residues

OTHER INFORMATION: 24 and 28 may be Trp or bromo-Trp

US-10-839-227-283
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40.0%; Pred. No. 1e+03;
tive 6; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 33; DB 5; Length 30; 60.0%; Pred. No. 9.5e+02; tive 4; Mismatches 0; Indels
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US-10-437-963-159510
PRIOR FILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: US 60/243,412
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-00-20
PRIOR FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: US 60/214,263
PRIOR PILING DATE: 2000-06-26
PRIOR FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 409
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 487, Application US/10351641; Publication No. US20030186874A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Conus geographus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 40.0
Matches 4; Conservative
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14 FKIGXXCCSG 23
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Best Local Similarity
Matches 6; Conserva
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US-10-351-641-487
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Aar41632 SSP for f Aar40873 SSP for f Aar40880 SSP for f Aar40880 SSP for f Aar40880 SSP for f Aar40880 SSP for f Aar40815 SSP for f Aar40875 SSP for f Aar40819 Conserved Ado5866 Conserved Ado5866 Conserved Aar408139 Gybear cy Aar408139 Gybear cy Aar408139 Gybear conserved Aar408139 Gybear conserved Aar408139 Gybear conserved Aar4123 Sequence Aar82090 Hepatitis Aar82090 Hepatitis Aar82090 Hepatitis Aar82090 Hepatitis	Abg75617 Arabidope Adv23624 HBV immun Adv23253 HBV immun Adv23253 HBV immun Adv23253 HBV immun Adv23253 HBV immun Adv23251 W.termina Adv2696 Human 5' Abj26710 Seed deve Adv12660 Signal pe Adv13661 Human inc Adw15123 Peptide e Adv13668 Erythropo Adw2692 Monomer 8 Adw16932 Monomer 8 Adw16932 Monomer 8 Adw16932 Monomer 8 Adw1693 Mory Adw1693 Mory Adw1693 Mory Adw1693 Monomer 8 Adw1693 Mory Adw1693 Mory Adw1693 Mory Adw1693 Monomer 8 Adw1693 Mory Adw1693 Mory Adw1693 Mory Adw1693 Monomer 8 Adw1690 Mory Adw1693 Mory Adw1693 Mory Adw1693 Monomer 8 Adw160 Mory Adw1	Adv90767 ATCYTP450 Adv90769 RABCYP4A61 Adv90769 RABCYP4A61 Adv62584 Cytochrom Ady62586 Cytochrom Ady62588 Cytochrom Ady62588 Cytochrom Ady62588 Cytochrom Ady62588 Cytochrom Ady62588 Cytochrom Ady62588 Cytochrom Ady6258 Aspergill Aab87038 Human TAN Aab87038 Human TAN Aab49519 Clone HCB Aau05874 Cone snai Aau05874 Cone snai Aau05874 Cone snai Aau05874 Cone snai Adm78214 Hepatitis
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GenCore version 5.1.7  Copyright (c) 1993 - 2006 Bioccel ein - protein search, using sw model March 8, 2006, 11:16:36; Search til (without 23:248 Mi e: US-10-751-235-14 e: 1 PXXGXXXCXG 10 table: BLOSUM62DXX - +two matrix callows table: Gapop 10.0, Gapext 0.5 d: 2443163 seqs, 439378781 residues umber of hits satisfying chosen parameters: DB seq length: 0	seq length: 2000000000 ssing: Minimum Match 0% Maximum Match 100% Listing first 100 summaries  A_Geneseq_21:* 1: geneseqp1980s:* 2: geneseqp2000s:* 4: geneseqp2001s:* 5: geneseqp2001s:* 6: geneseqp2001s:* 7: geneseqp2001s:* 8: geneseqp2001s:* 9: geneseqp2001s:* 10: geneseqp2001s:* 10: geneseqp2000s:* 10:	33 1000.0

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neuroleptic; antimanic; cerebroprotective; immunomodulatory; antimanic artimanic; cerebroprotective; immunomodulatory; haemostatic; antimination; anti-microbial; cardiant; cytostatic; antimination; haemostatic; anticonvulsant; vasotropic; vaccine; gene therapy; anti-sense therapy; neural; reproductive; immune disorder; immunodeficiency; infection; aneurysm; demyelinating disease; autoimmunity; cancer; inflammation; aneurysm; haemorrhage; Alzheimer's disease; Parkinson's disease; Huntington's disease; Tourette syndrome; multiple sclerosis; meningitis; ischaemia; mania; dementia; obsessive compulsive disorder; viral prophylaxis; developmental disorder; sexually-linked disorder; cardiovascular disorder; food additive; preservative; chromosome 11.
                     Human secreted protein sequence encoded by gene 3 SEQ ID NO:129
                                                 secreted protein; diagnosis; neuroprotective; nootropic;
                                                                                                                                                                                                                                                                         99WO-US019330.
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98US-0098634P.
                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC.
29-JUN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                         Lafleur DW,
                                                                                                                                                                                                                                                                                                                                                              Ruben SM,
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                         24-AUG-1999;
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Soppet DR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention provides new DNA molecules (AAX60773-X60781) encoding soybean cytochrome P450 enzymes (AAX09183-Y09191) respectively. The DNA encoding the cytochrome P450 enzymes is useful for transformation of Solanaceae crop plants. Transgenic plants comprising DNA constructs having the P450 encoding nucleic acid sequences are resistant to phenylurea herbicides. The transgenic plants have increased resistance to phenylurea herbicides compared to wild-type plants of the same species. The plant crops, e.g. turfgrass, tobacco, potato, tomato, corn, rice, cotton, soybean, rape, wheat, oats, barley or rice are particularly resistant to fluometuron, linuron, chlortoluron or diuron
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  Core
Core
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Aay89129 (
Aay89127 (
Aay89163 (
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                                                                                                                                                                                                  Soybean cytochrome P450 enzyme conserved peptide motif.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding soybean cytochrome P450 enzymes.
                                                               ALIGNMENTS
 AAY89129
AAY89127
AAY89163
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                                                                                                                          AAY09193 standard; peptide; 10 AA.
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Best Local Similarity 100.
Matches 10; Conservative
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AAY91408
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Duan RD;

sen HS, Shi Y, Rosen CA, Florence KA; Endress GA, Ebner R, Komatsoulis G, I

Olsen HS,

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The polymuclectide sequences given in AAA26281 to AAA26336 encode the human secreted proteins given in AAY91346 to AAY91449. The human secreted proteins given in AAY91346 to AAY91449. The human secreted proteins given in AAY91346 to AAY91449. The human secreted corrections can have activities based on the tissues and cells they are expressed in. Examples of the activities are: neuroprotective, nootropic, neuroleptic; antimanic; cerebroprotective; immunomodulatory; anti-corrections and vasotropic. The polymucleotides and proteins may be used to prevent, treat or ameliorate a medical condition, e.g. by protein correction repeated to proteins of the invention include neural, reproductive, or immunodeficiency, infection, lymphomas, demyelinating diseases, auto-include neural, reproductive, or immunodeficiency, inflammation, aneurysms and haemorrhages. Specific examples include: Alzheimer's disease; compulsive disorder and viral prophylaxis. The polymucleotides and proteins can also be used in the detection of disorders associated with the function of the protein, for example, the detection of developmental disorders, sexually-linked disorders, mania; proteins can also be used in the detection of developmental consorders, sexually-linked disorders, or disorders of the cardiovascular system. They may also be used as food additives or preservatives.
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Novel secreted proteins and corresponding DNA molecules that can be used to prevent, treat and diagnose disease in humans, for example, Alzheimer's, cancer, and immune disorders.
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                                                                                                                                                                                                Disclosure; Page 390; 416pp; English.
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Cytochrome P450 1B1; CYP1B1; cancer; immunotherapy; diagnosis; HLA; human leukocyte antigen; cytotoxic T-lymphocyte; CTL; MHC; APC; major histocompatibility complex; antigen presenting cell; melanoma; Lymphoma; carcinoma; multiple myeloma; leukaemia.

AAM13360 standard; peptide; 10 AA.

RESULT 4

(first entry)

09-OCT-2001

AAM13360;

HLA-A26 decamer #423

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The present invention describes a method for treating a patient having, or is at risk of having, a cell expressing cytochrome P450 IBI (CYDIBI), which involves administering to the patient a cytocoxic T-lymphocyte complex kills the cell, an antigen presenting cell (APC) that cell, an antigen presenting cell (APC) that cell, an antigen presenting cell (APC) that cerivates CTL, a peptide of CYPIBI that binds to major histocompatibility complex (MFC) molecule, or a nucleic acid molecule encoding CYPIBI or peptide of CYPIBI or a peptide of CYPIBI that binds to method for assessing the level of immunity of a patient to CYPIBI or a peptide of CYPIBI that binds to mic complex molecule, involving measuring the level of CTL specific for CYPIBI or the peptide of CYPIBI in a sample from the patient or specific of a MFC complex molecule, (I) that binds to MFC complex molecule, (3) an exvivo generated CTL (II) that specifically kills a cell expressing CYPIBI or a specific of a MFC complex-restricted feashon; and (4) an exvivo generated APC (III) that presents a peptide of a CYPIBI in the context of a wHC complex molecule. The method is useful for treating a patient is useful for the prevention, treatment and diagnosis of cancer, e.g. melanoma, lymphoma, carcinoma, sarcoma, multiple myeloma, leukemia, and brain cancer. AAN06905 to AAM1366 represent CYPIBI peptides which can brain cancer and not the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Treating a cancer patient involves administering to patient a cytotoxic T-lymphocyte, an antigen presenting cell that activates T cells, a peptide of cytochrome P450 1B1, or a polynucleotide encoding the peptide.
                                                                                                                                                                                                     Cytochrome P450 1B1; CYP1B1; cancer; immunotherapy; diagnosis; HLA; human leukcoyte antigen; cytocoxic T-lymphocyte; CT1, MHC; APC; major histocompatibility complex; antigen presenting cell; melanoma; lymphoma; carcinoma; sarcoma; multiple myeloma; leukaemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (DAND ) DANA FARBER CANCER INST INC. (UYBO-) UNIV BOSTON.
                                      AAM10370 standard; peptide; 10 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schultze JL, Vonderheide RH,
Von Bergwelt- Baildon M;
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                                                                                                                      (first entry)
                                                                                                                                                               HLA-B *0702 decamer #320.
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Best Local Similarity
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                                                                              AAM10370;
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Matches
                RESULT 3
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Treating a cancer patient involves administering to patient a cytotoxic T -lymphocyte, an antigen presenting cell that activates T cells, a peptide of cytochrome P450 1B1, or a polynucleotide encoding the peptide.

Maecker B;

Nadler LM,

Schultze JL, Vonderheide RH, Sherr D, Von Bergwelt- Baildon M;

NPI; 2001-355537/37.

(DAND ) DANA FARBER CANCER INST INC. (UYBO-) UNIV BOSTON.

99US-0165590P.

15-NOV-1999;

15-NOV-2000; 2000WO-US031513.

40200135810-A2

25-MAY-2001

Homo sapiens.

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The present invention describes a method for treating a patient having, or is at risk of having, a cell expressing cytochrome P450 1B1 (CYP1B1), which involves administering to the patient a cytocoxic T-lymphocyte (CTL) that kills the cell, an antigen presenting cell (APC) that cerivates CTL, a peptide of CYP1B1 that binds to major histocompatibility complex (MHC) molecule, or a nucleic acid molecule encoding CYP1B1 or complex (MHC) molecule, or a nucleic acid molecule encoding CYP1B1 or complex (MHC) molecule, no a patient to CYP1B1 or a peptide of CYP1B1 that level of immunity of a patient to CYP1B1 or a peptide of CYP1B1 that binds to MHC complex molecule, involving measuring the level of CTL specific for CYP1B1 or the peptide of CYP1B1 in a sample from the patient; (1) a cyP1B1 peptide (1) that binds to MHC complex molecule; (3) an exvivo generated APC (III) that specifically kills a cell expressing CYP1B1 in a specific of a MHC complex-restricted fashion; and (4) an exvivo generated APC (III) that presents a peptide of a CYP1B1 in the context of a MHC complex molecule. The method is useful for treating a patient having or is at risk of having a cell that expresses CYP1B1. The method is useful for the prevention, treatment and diagnosis of cancer, e.g.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           melanoma, lymphoma, carcinoma, sarcoma, multiple myeloma, leukemia, and lung, ovarian, uterine, cervical, prostate, liver, colon, pancreatic and brain cancer. Amolegos to Amilisce represent CYPIBI peptides which can bind to human leukcoyte antigens (HLAB), as well as other amino acid sequence used in the exemplification of the present invention
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Pred. No. 3.5e+02;
6; Mismatches 0; Indels
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Similarity 40.0%; E
4; Conservative 6;
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Best Local Similarity
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4; Conservative FXXGXXXCXG 10 |::|:::|:| FSVGKRRCIG 10

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Cytochrome P450 1B1; CYP1B1; cancer; immunotherapy; diagnosis; HLA; human leukocyte antigen; cytotoxic T-lymphocyte; CTL; MHC; APC; major histocompatibility complex; antigen presenting cell; melanoma; lymphoma; carcinoma; sarcoma; multiple myeloma; leukaemia.

AAM10626 standard; peptide; 10 AA.

(first entry)

09-OCT-2001

AAM10626;

HLA-A \*0201 decamer #409.

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RESULT 6
AAM10626
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytochrome P450 1B1; CYP1B1; cancer; immunotherapy; diagnosis; HLA; human leukocyte antigen; cytotoxic T-lymphocyte; CTL; MHC; APC; major histocompatibility complex; antigen presenting cell; melanoma; lymphoma; carcinoma; sarcoma; multiple myeloma; leukaemia.
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                                                                                                 AAM09243 standard; peptide; 10 AA.
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Von Bergwelt- Baildon M;
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                                                                                                                                                                                                                                                                                 (first entry)
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Best Local Similarity
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(UYBO-) UNIV
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                                                            AAM09243
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Sherr D, Nadler LM,

(DAND ) DANA FARBER CANCER INST INC. (UYBO-) UNIV BOSTON.

15-NOV-2000; 2000WO-US031513

WO200135810-A2.

25-MAY-2001.

Homo sapiens.

99US-0165590P

15-NOV-1999;

Schultze JL, Vonderheide RH, Von Bergwelt- Baildon M;

WPI; 2001-355537/37.

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The present invention describes a method for treating a patient having, or is at risk of having, a cell expressing cytochrome P450 IB1 (CYPIB1), which involves administering to the patient a cytocoxic T-lymphocyte (CTL) that kills the cell, an antique presenting cell (APC) that activates CTL, a peptide of CYPIB1 that binds to major histocompatibility complex (MMC) molecule, or a nucleic acid molecule encoding CYPIB1 or peptide of CYPIB1. Also described are: (1) a method for assessing the level of immunity of a patient to CYPIB1 or a peptide of CYPIB1 that binds to MHC complex molecule, involving measuring the level of CTL specific for CYPIB1 peptide (I) that binds to MHC complex molecule, involving measuring the level of CTL specific for CYPIB1 peptide (I) that binds to MHC complex molecule; (3) an exvivo specific of a MHC complex restricted fashion; and (4) an exvivo cyvivo generated APC (III) that presents a peptide of a CYPIB1 in the context of a MHC complex molecule. The method is useful for treating a patient complex molecule. The method is useful for treating a patient of is useful for the prevention, treatment and diagnosis of cancer, e.g. melanoma, lymphoma, carcinoma, sarcoma, multiple myeloma, leukemia, and clumg, ovarian, uterine, cervical, prostate, liver, colon, pancreatic and chain cancer. AAM06905 to AAM3356 represent CYPIB1 peptides which can bind to human leukocyte antigens (HLAs), as well as other amino acid sequence used in the exemplification of the present invention
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Pred. No. 3.5e+02;
6; Mismatches 0; Indels
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Cloning; characterisation; human; cytochrome P450; CYP 27C1; cytostatic; thyromimetic; antidiabetic; antipsoriatic; tuberculostatic; osteopathic; demaclogical; antilipsemic; gene therapy; vaccine; Vitamin D; diabetes; vitamin D metabolite deficiency; hyporparathyroidism; pyoparathyroidism; medullary carcinoma; psoriasis; sarcoidosis; tuberculosis; osteomalacis; chronic renal disease; vitamin D dependent rickts; anticonvulsant; fibrogenesis imperfects ossium; osteititis fibrosa cysticis; osteoporosis; osteoporosis; osteoporosis; osteoporosis; osteoporosis; osteoporosis; dilopathic hypercalcaemia; tropical sprue; malabsorption syndrome; cholesterol steroid; lipid metabolic disorder.
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                                                                                                                                                                                                                                                                                                              Conserved haem region generic peptide.
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                                                                          ABP53084 standard; peptide; 10 AA.
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RESULT
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fibrosa cystica, osteomalacia, osteoporosis, osteopaenia, osteosclerosis, renal osteodystrophy, rickets, glucocorticoid antagonism, idiopathic

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hypercalcaemia, malabsorption syndrome, steatorrhoea, and tropical sprue, or cholesterol, steroid and other lipid metabolic disorders. The present sequence represents a conserved haem region generic peptide, which is used in an example from the present invention
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100.0%; Pred. No. 3.5e+02;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Aspergillus ochraces in alpha hydroxylase protein), oxidoreductases and polynucleotides encoding such proteins. Host cells comprising the sequences of the invention are useful for making one or more enzymes from the metabolic pathway for the synthesis of sitosterol to eplerenone. They are useful for selective oxidation of a compound to an hydroxylated product. Compositions of the invention are useful for producing spores
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renal osteodystrophy, rickets, glucocorticoid antagonism, idiopathic hypercalcaemia, malabsorption syndrome, steatorrhoea, and tropical sprue, or cholesterol, steroid and other lipid metabolic disorders. The present sequence represents a CYP 2/Cl haem-binding signature peptide, which is used in an example from the present invention
                                                                                                    Gaps
                                                                                                                                                                                                                                                                                  steroid bioconversion, antiinflammatory, antiarthritic; cytostatic; cardiant; cytochrome P450; oxidoreductase; haem binding motif.
                                                                                                                                                                                                                                                                         alpha hydroxylase; enzyme; sitosterol; eplerenone; cell therapy;
                                                                                                                                                                                                                                                     Aspergillus ochraceus cytochrome p450 conserved haem binding motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present invention relates to novel cytochrome P450-like enzyme
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Pred. No. 3.5e+02;
6; Mismatches 0;
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CLAYTON R.
                                                                                Query Match
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from A. ochraceus, A. niger, A. nidulans, Rhizopus oryzae, R. stolonifer, R. arrhizus Trichothecium roseum, Fusarium oxysporum and M. olivaceum etc., preferably to produce spores from A. ochraceus. Sequences of the invention are useful in bioconversion of steroid substances to their 11 alpha-hydroxy counterparts. They are also used in cell therapy. The present sequence is A. ochraceus cytochrome p450 conserved haem binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to the isolation of cotton (+)-delta-cadinene 8-hydroxylase (designated as CYP706B1), and the polynuclectide sequence encoding it. The CYP706B1 protein is a cytochrome P450 which is useful as a target for suppression of the biosynthesis of gossypol and related sesquiterpenes in cotton seeds through genetic engineering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel cotton (+)-gamma-cadinene 8-hydroxylase polypeptide designated as CYP706B1, useful as target for suppression of biosynthesis of gossypol formation in cotton seeds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            biosynthesis of gossypol; sesquiterpene; cotton seed; cotton cultivate; sesquiterpenoid; livestock feed; monooxygenase; haem-binding motif.
                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conserved haem-binding motif found in eukaryotic P450 monooxygenases
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                                                                                                                                                                                                                                                                                             Length 10;
                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                Score 33; DB 5; I
Pred. No. 3.5e+02;
                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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note= "Any amino acid"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-FEB-2002; 2002US-00067534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-FEB-2001; 2001US-0267160P.
                                                                                                                                                                                                                                                                                                                          Local Similarity ....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note=
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CHEN X.
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                                                                                                                                                                                                                                                                                                                                                                                                            1 FXXCXXXCXG
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Unidentified.
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                                                                                                Query Match
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Matches
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Matches
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techniques. The polymucleotide sequence encoding CYP706B1 is useful in suppression of the biosynthesis of gossypol and related sesquiterpenes in cotton seeds, where the polymucleotide sequence is expressed in antisense or sense orientation as a perfect match to the native gene whose or sense orientation as a perfect match to the native gene whose invention is suggit to be suppressed. The polymucleotide sequence of the invention is useful for producing cotton cultivates which avoid the presence of sesquiterpenoids in their seeds, and for producing cotton humans. The present sequence represents a highly conserved haem-binding motif found in eukaryotic P450 monooxygenases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New Rhodococcus ruber nucleic acid, useful for transforming bacteria for depolluting soil contaminated with ethyl tert-butyl ether comprises the cytochrome P-450 gene cluster involved in cleavage of ethyl tert-butyl
                                                                                                                                                                                                                                                                                                                                                  Cytochrome P450; EthB; ether; ethyl tert-butyl ether; ETBE; degradation;
bioremediation; soil decontamination; pollutant; biosensor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is a consensus motif of chytochrome P450s, and includes a Cys residue that is strictly conserved in all cytochrome P450s. The motif has been identified in the EthB protein (see ABR42001)
                                                                                                                                                                Gaps
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                                                                                                                                         100.0%; Score 33; DB 6; Length 10; 90.0%; Pred. No. 3.5e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      note= "any amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "any amino acid"
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                                                                                                                                                                                                                                                              ABR42010 standard; peptide; 10 AA.
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                                                                                                                                                                                                                                                                                                                              Cytochrome P450 conserved motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-JUN-2001; 2001EP-00401667.
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                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                  Local Similarity 90.
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                                                                                                                                                                                               1 PXXGXRXCXG 10
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(INSP ) INST FRANCAIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Miras I,
                                                                                                                                                                                   1 PXXGXXXCXG
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                                                                                                                                                                                                                                                                                                                                                                        Rhodococcus ruber.
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                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                    Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chauvaux S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EP1270722-A1
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                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                   ABR42010;
                                                                                                                                          Query Match
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of Rhodococcus ruber strain CNCM I-1889 cells. EthB is an ethyl textbutyl ether (ETBB)-induced cytochrome P450. It forms part of a cytochrome P450 system involved in the cleavage of ether fuel additives. Recombinant host cells comprising a vector encoding eth genes, and which are capable of ETBE degradation or mineralization, can be used for bloremediation of a contaminated soil or effluent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated P450RAI-3 nucleic acid molecule and polypeptide, useful for diagnosing, preventing, or treating disorders with aberrant expression or activity of the P450RAI-3, such as cancer, actinic keratosis, acne and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, retinoic acid, vitamin A; cytochrome P450; actinic Keratosis, P450RAI; cancer; psoriasis; acne; ichthyosis; gene therapy; vaccine;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 10;
                                                                                                                                                                                                                                                                              Length 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytochrome P450 putative family signature peptide #2
                                                                                                                                                                                                                                                                              ; Score 33; DB 6; L
Pred. No. 3.5e+02;
2; Mismatches 0;
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Pred. No. 3.5e+02;
6; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE35263 standard; peptide; 10 AA.
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                                                                                                                                                                                                                                                                                 100.001
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Μ.
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                                                                                                                                                                                                                                                                                                              80.08;
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                                                                                                                                                                                                                                                                                                                                              8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CYTO-) CYTOCHROMA INC.
                                                                                                                                                                                                                                                                                                                                                                                                          1 FXXGXXXCXG 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 FXXGXXXCXG 10
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                                                                                                                                                                                                                        Sequence 10 AA;
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RESULT 13

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**AAE35262** 

enzyme.

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The polypeptide of the invention demonstrates antipsoriatic and osteopathic activities and may be useful for identifying compounds which modulate the activity or inhibit the expression of vitamin-D3 hydroxylase and thus for treating or preventing hypercalcaemia. Furthermore, the polypeptide may be utilised during gene and antisense therapy, as well as for treating activated vitamin-D3 deficiency disorders such as hypoparathyroidism, rickets, psoriasis, osteoporosis and renal insufficiency. The current sequence is that of the peptide 1 of the invention which is related to human vitamin-D3 hydroxylase.
                                                                                                           vitamin-D3 hydroxylase; VDDH; antipsoriatic; osteopathic; hypercalcaemia; gene therapy; antisense; hypoparathyroidism; rickets; psoriasis; osteoporosis; renal insufficiency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vel vitamin-D3 hydroxylase protein, useful for identifying modulators the vitamin-D3 hydroxylation activity of the enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a novel vitamin-D3 hydroxylase (VDDH) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ecdysteroid synthesis inhibitor; insecticidal; cytochrome P450; haem ligand motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 33; DB 7; Length 10
Pred. No. 3.5e+02;
6; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytochrome P450 haem ligand signature motif peptide.
                                                                          Peptide 1 related to human vitamin-D3 hydroxylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2. .3
/label= OTHER
/note= "OTHER = Any amino acid"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 10; 18pp; Japanese.
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(HERI-) HERIKKUSU KENKYUSHO KK.
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                                                                                                                                                                                                                                                                                                                                                           08-AUG-2001; 2001JP-00241396.
                                                                                                                                                                                                                                                                                                                    08-AUG-2001; 2001JP-00241396.
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                                       18-DEC-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 FXXGXXXCXG 10
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference 2
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                                                                                                                                                                                                Unidentified
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                                                                                                                                                                                                                                                                              18-FEB-2003
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ADC56716;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to retinoic acid metabolising cytochrome P450, P450RAI polypeptides and polymucleotides. Methods and compositions of the invention are useful for diagnosing, preventing, ameliorating and/or treating disorders associated with the aberrant expression or activity of the P450RAI such as diseases related to vitamin A and retinoic acid metabolism, e.g. cancer, actinic keratosis, psoriasis, acne and ichthyosis. The invention is useful in gene therapy and as vaccine. The present sequence is cytochrome P450 putative family signature peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated P450RAI-3 nucleic acid molecule and polypeptide, useful for diagnosing, preventing, or treating disorders with aberrant expression or activity of the P450RAI-3, such as cancer, actinic keratosis, acne and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                            Human, retinoic acid, vitamin A, cytochrome P450, actinic keratosis,
P450RAI, cancer, psoriasis, acne, ichthyosis, gene therapy, vaccine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This peptide is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 33; DB 6; Length 10; 100.0%; Pred. No. 3.5e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                       Cytochrome P450 putative family signature peptide #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wisniewski J, Petkovich PM, Ramshaw H;
                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 72; 231pp; English.
                                                                                                   AAE35262 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                        . .3
label= Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                              5. .7
/label= Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-MAY-2002; 2002WO-CA000758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-MAY-2001; 2001US-0292531P
                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 FXXGXXXCXG 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10
    1 FGGGARSCLG 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CYTO-) CYTOCHROMA INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-112152/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FXXGXXXCXG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200295034-A2
                                                                                                                                                                                                                                                                                                                                          Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
                                                                                                                                                                               28-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-NOV-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 psoriasis.
                                                                                                                                          AAE35262;
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Gaps

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5..7 /label= OTHER

Misc-difference 5

ADC56716 standard; peptide; 10 AA.

RESULT 14

ADC56716 ID ADC5 XX

Best Local Matches 1

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The present invention relates to genes, proteins and methods comprising carotemoid monoxygenases in the cytochrome P450 family. The invention also relates to altering carotemoid ratios in plants and microorganisms using LUT1 epsilon-hydroxylases and/or CYP97A beta-hydroxylases. The invention is useful in altering the carotemoid production in a plant for enhancing production of specific carotemoid compounds that are potent antioxidants. The present sequence is thale cress LUT1 cytochrome P450 monooxygenase cysteine motif peptide.
                                                                                                                                                a nucleic acid sequence encoding a P450 activity, useful in altering the for enhancing production of specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Xaa may be any naturally occurring amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Xaa may be any naturally occurring amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cytochrome P450 monooxygenase cysteine consensus motif, SEQ ID NO: 14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Xaa may be any naturally occurring amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pigment; metabolic engineering; antioxidant; transgenic plant; cytochrome P450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 33; DB 9; L. Pred. No. 3.5e+02; 6; Mismatches 0;
                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 15; 135pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                       polypeptide having monocxygenase l carotenoid production in a plant f carotenoid compounds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AEB16916 standard; peptide; 10 AA.
                                                                  Kim J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
40.0%; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kim J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-JAN-2004; 2004US-00751235.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-JAN-2004; 2004US-00751235.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2. .3
/note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note=
                                                                Tian L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tian L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |::|::|:|
1 FSGGPRKCVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 FXXGXXXCXG
                                                                                                     WPI; 2005-487984/49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2005-487984/49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (DELL/) DELLAPENNA (TIAN/) TIAN L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
(TIAN/) TIAN L. (KIMJ/) KIM J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US2005150002-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10 AA;
                                                                Dellapenna D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ь.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dellapenna D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-SEP-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AEB16916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KIMJ/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AEB16916
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ecdysteroid synthesis comprising contacting an ecdysteroid biosynthetic enzyme with a candidate inhibitor molecule and determining whether or not said inhibitor inhibits enzymatic activity. The enzyme comprises a novel 1solated polypeptide of CYP302a1, CYP306a1, CYP307a1, CYP314a1 or CYP315a1. The method of the invention may be useful for determining whether or not a molecule has insecticidal properties and for making inhibitors of ecdysteroid synthesis. The current sequence is that of the cytochrome P450 haem ligand signature motif peptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LUT1 cytochrome P450 monooxygenase cysteine motif peptide, SEQ ID NO: 15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention relates to a novel method for identifying inhibitors of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polypeptide useful for identifying inhibitors of ecdysteroid thesis, determining insecticidal properties, and making an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pigment, metabolic engineering, antioxidant, transgenic plant; cytochrome P450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 33; DB 7; Length 10; 100.0%; Pred. No. 3.5e+02; ive 0; Mismatches 0; Indels
/note= "OTHER = Any amino acid"
                                     /label= OTHER
/note= "OTHER = Any amino acid"
                                                                                                                                                                                                                                                                                                                                                                                 Warren JT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AEB16917 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 3; 21pp; English
                                                                                                                                                                                                                               07-SEP-2001; 2001US-0317890P
07-SEP-2001; 2001US-0318006P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-JAN-2004; 2004US-00751235.
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                                                                                                                                                                                     06-SEP-2002; 2002US-00236433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                               O'connor M, Gilbert LI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FXXGXXXCXG 10
                                                                                                                                                                                                                                                                                           GILBERT L I. WARREN J T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (DELL/) DELLAPENNA D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-777312/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 10; Conserv
                 Misc-difference 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US2005150002-A1.
                                                                                                     US2003100025-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  insecticide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-SEP-2005
                                                                                                                                                29-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-JUL-2005
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                                                                                                                                                                                                                                                                                         (OCON/)
(GILB/)
(WARR/)
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RESULT AEB1691

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Gaps

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Length 10; Indels

Gaps

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Length 11; Indels

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cytochrome P450 homologues pCGP142 and pCGP147 was used to design synthetic PCR primers. The primers may be used in PCR for amplification of petal cytochrome P450 homologues. See also AAR30868-75. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                ; Score 33; DB 2; L. Pred. No. 3.9e+02; 3; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shimada Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11; Page 58; 82pp; Japanese.
                                                                                                                                                                                                              AAR40877 standard; protein; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92JP-00044963.
                                                                                  100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (KYOW ) KYOWA HAKKO KOGYO CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                    92WO-JP001520.
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                                                                                             70.08;
                                                                                                                                                                                                                                                                                     (first entry)
                                                                                 Query Match
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kiyokawa S,
                                                                                                                               1 FXXGXXXCXG 10
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FGXGXRXCPG 11
                                                                                                                                                                                                                                                             (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1993-303469/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                             Petunia x hybrida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAQ47878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11 AA;
                                                             Sequence 11 AA;
                                                                                                                                                                                                                                                            24-OCT-2003
25-MAR-2003
28-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                       WO9318155-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kikuchi Y,
Okinaka Y;
                                                                                                                                                                                                                                                                                                                                                                                                                             16-SEP-1993
                                                                                                                                                                                                                                        AAR40877;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                           RESULT 19
                                                                                                                                                                                                      AAR40877
ID AAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid sequence encoding a di:hydro:kaempferol-hydroxylating enzyme - e.g. cytochrome P450 introduced into transgenic plants for controlling flavonoid pigmentation in plants and organisms.
                                                                                 The present invention relates to genes, proteins and methods comprising carotenoid monooxygenases in the cytochrome P450 family. The invention also relates to altering carotenoid ratios in plants and microorganisms using LuTI epsilon-hydroxylases and/or CYP97A beta-hydroxylases. The invention is useful in altering the carotenoid production in a plant for enhancing production of specific carotenoid compounds that are potent antioxidants. The present sequence is a cytochrome P450 monooxygenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The consensus sequence of haem-binding domains for advocado and petunia
                 the
   New expression vector comprising a nucleic acid sequence encoding a polypeptide having monooxygenase P450 activity, useful in altering the carotenoid production in a plant for enhancing production of specific carotenoid compounds.
                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                    pigmentation; colour; amplification;
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                                                                                                                                                                                                                  Length 10;
                                                                                                                                                                                                               100.0%; Score 33; DB 9; Length 10
100.0%; Pred. No. 3.5e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lester
                                                                                                                                                                                                                                                                                                                                                                                                                              Consensus haem-binding domain of cyt-P450 in plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tanaka Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytochrome P450; advocado; petunia; ss.
                                                             SEQ ID NO 14; 135pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kovacic F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                AAR30867 standard; protein; 11 AA
                                                                                                                                                                    cysteine consensus motif peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'label= Ala, Ser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'label= Lys, Arg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Ile, Gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ITFL-) INT FLOWER DEV PTY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dihydrokaempferol, flavonoid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91AU-00007173.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92EP-00306379
                                                                                                                                                                                                                                                                                                                                                                                            (revised)
(first entry)
                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cornish EC,
                                                                                                                                                                                                                                                                1 FXXGXXXCXG 10
                                                                                                                                                                                                                                                                                      FXXGXXXCXG 10
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                                                                                                                                                                                                                          1 Similarity
10; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                            Sequence 10 AA;
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17-FEB-1992;
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12-MAY-1993
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                                                             Claim 7;
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                                                           Flavonoid-3',5'-hydoxylase; transformation; plants; petunia; rose; tobacco; pigment alteration; blue; SSP; single specific primer; PCR; polymerase chain reaction; amplification; expression; ss.
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Pred. No. 3.9e+02;
6; Mismatches 0; Indels
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SSP for flavonoid-3',5'-hydroxylase gene product.
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Insertion of the sequences (AAQ47840-42) into plants such as rose, petunia, tobacco and carnation, using a suitable vector such as agrobacteratium, give transformed plants which express the gene, resulting in petals with a bluer colour than normal, and/or pigmentation patterns which do not occur naturally. The sequences were amplified using primers (AAQ47843-70). Related single specific primers using a gene sequence coding for the haem-binding region of cytochrome P450 are shown in (AAQ47871-Q47903). (Updated on 25-MAR-2003 to correct PN field.) (Updated on 24-OCT-2003 to standardise OS field)
                                                                         Plavonoid-3',5'-hydoxylase; transformation; plants; petunia; rose; tobacco; pigment alteration; blue; SSP; single specific primer; PCR; polymerase chain reaction; amplification; expression; ss.
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                                                                                                                                                                                                                                                                                                                                                                                      Shimada R;
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Okinaka Y;
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                                       SSP for flavonoid-3',5'-hydroxylase gene
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   28-MAR-1994 (first entry)
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2 FGVGLRMCPG 11
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                      Petunia x hybrida.
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25-MAR-2003
28-MAR-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene coding for flavonoid-3',5'-hydroxylase of petunia petals - used to transform plants e.g. petunia, rose or tobacco to give bluer flower colour and altered pigment pattern.
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                                                                                                              AAR40874 standard; protein; 11 AA.
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Best Local Similarity 40.0%,
Best Acad 4; Conservative
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FGGGPRRCPG 11
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N-PSDB; AAQ47875.
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FGSGRRSCPG
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25-MAR-2003
28-MAR-1994
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25-MAR-2003
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Okinaka Y;
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FGAGRRICPG 11
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N-PSDB; AAQ47873
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Okinaka Y;
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25-MAR-2003
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                                                                                                                                      Gene coding for flavonoid-3',5'-hydroxylase of petunia petals - used to transform plants e.g. petunia, rose or tobacco to give bluer flower colour and altered pigment pattern.
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                                                                              Shimada
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                                                                              Ohbayashi M,
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FGSGFCSCPG 11
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Matches 4; Conserv
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25-MAR-2003
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Okinaka Y;
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to give bluer flower
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Gene coding for flavonoid-3',5'-hydroxylase of petunia petals - use transform plants e.g. petunia, rose or tobacco to give bluer flower colour and altered pigment pattern.
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                                                                                                                                                          Claim 11; Page 56; 82pp; Japanese.
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Gene coding for flavonoid-3',5'-hydroxylase of petunia petals - used transform plants e.g. petunia, rose or tobacco to give bluer flower colour and altered pigment pattern.
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                                                                                                                                                                                                                                                                            SSP for flavonoid-3',5'-hydroxylase gene product.
                                                                                                                                 AAR41634 standard; protein; 11 AA.
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         1 FXXGXXXCXG 10
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                                                                                                                                                                                                         (revised)
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FGAGRRICAG 11
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25-MAR-2003
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Okinaka Y;
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which do not occur naturally. The sequences were amplified using primers (AAQ47843-70). Related single specific primers using a gene sequence coding for the haem-binding region of cytochrome P450 are shown in (AAQ47871-047903). (Updated on 25-MAR-2003 to correct PN field.) (Updated on 24-OCT-2003 to standardise OS field)
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                                                                                                                           Score 33; DB 2; Length 11.
Pred. No. 3.9e+02;
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                                                                                                                                                                                    6; Mismatches
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40.0%; P
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FGVGPKMCPG 11
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Best Local Similarity
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Best Local Similarity
Matches 4; Conserv
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                                                                                                              Sequence 11 AA;
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Shimada

Ohbayashi M,

Shimada Y,

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                                                                                        petunia, tobacco and carnation, using a suitable vector such as agrobacterium, give transformed plants which express the gene, resulting in petals with a bluer colour than normal, and/or pigmentation patterns which do not occur naturally. The sequences were amplified using primers (AAQ47843-70). Related single specific primers using a gene sequence coding for the haem-binding region of cytochrome P450 are shown in (AAQ47871-Q47903). (Updated on 25-MAR-2003 to correct PN field.) (Updated on 24-OCT-2003 to standardise OS field),
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                                                             Insertion of the sequences (AAQ47840-42) into plants such as rose,
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Pred. No. 3.9e+02;
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Claim 11; Page 61; 82pp; Japanese.
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Insertion of the sequences (AAQ47840-42) into plants such as rose, petunia, tobacco and carnation, using a suitable vector such as agrobacterium, give transformed plants which express the gene, resulting in petals with a bluer colour than normal, and/or pigmentation patterns which do not occur naturally. The sequences were amplified using primers (AAQ47843-70). Related single specific primers using a gene sequence coding for the haem-binding region of cytochrome P450 are shown in (AAQ47871-Q47903). (Updated on 25-WAR-2003 to correct PN field.) (Updated on 24-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                            Gene coding for flavonoid-3',5'-hydroxylase of petunia petals - used to transform plants e.g. petunia, rose or tobacco to give bluer flower
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                                                                                                                                                                Ohbayashi M, Shimada R;
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40.0%; Pred. No. 3.9e+02;
iive 6; Mismatches 0;
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                                                                                                                                                                                                                                                                                                  transform plants e.g. petunia, rose
colour and altered pigment pattern.
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Okinaka Y;
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FGVGRRSCPG 11
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Best Local Similarity
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28-MAR-1994
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               16-SEP-1993
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Okinaka
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                                                                                      Flavonoid-3',5'-hydoxylase; transformation; plants; petunia; rose; tobacco; pigment alteration; blue; SSP; single specific primer; PCR; polymerase chain reaction; amplification; expression.
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                                                      SSP for flavonoid-3',5'-hydroxylase gene product.
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28-MAR-1994
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in petals with a bluer colour than normal, and/or pigmentation patterns which do not occur naturally. The sequences were amplified using primers (AAQ47843-70). Related single specific primers using a gene sequence coding for the hame-binding region of cytochrome P450 are shown in (AAQ47871-Q47903). (Updated on 25-WAR-2003 to correct PN field.) (Updated on 24-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Insertion of the sequences (AAQ47840-42) into plants such as rose, petunia, tobacco and carnation, using a suitable vector such as agrobacterium, give transformed plants which express the gene, resulting in petals with a bluer colour than normal, and/or pigmentation patterns which do not occur naturally. The sequences were amplified using primers (AAQ47843-70). Related shingle specific primers using a gene sequence coding for the haem-binding region of cytochrome P450 are shown in (AAQ4781-Q47903). (Updated on 25-MAR-2003 to correct PN field.) (Updated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Flavonoid-3',5'-hydoxylase; transformation; plants; petunia; rose; tobacco; pigment alteration; blue; SSP; single specific primer; PCR; polymerase chain reaction; amplification; expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 33; DB 2; Length 11;
Pred. No. 3.9e+02;
Mismatches 0; Indels
                                                                                                                                                                                  Length 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ohbayashi M,
                                                                                                                                                                                  ; Score 33; DB 2; L
Pred. No. 3.9e+02;
6; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSP for flavonoid-3',5'-hydroxylase gene product.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11; Page 55; 82pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                             AAR40871 standard; protein; 11 AA.
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40.0%; F
                                                                                                                                                                                  100.08;
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                                                                                                                                                                                                                          4; Conservative
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FGSGRRICPG
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                                                                                                                                                                                                     Local Similarity
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Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Petunia x hybrida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAQ47872
                                                                                                                                            Sequence 11 AA;
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28-MAR-1994
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Okinaka Y;
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                                                                                                                                                                                    Query Match
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Matches
                                                                                                                                                                                                                                                                                                                                                                   RESULT 31
    8888888
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                                                                                                                                                                            Insertion of the sequences (AAQ47840-42) into plants such as rose, petunia, tobacco and carnation, using a suitable vector such as agrobacterium, give transformed plants which express the gene, resulting in petals with a bluer colour than normal, and/or pigmentation patterns which do not occur naturally. The sequences were amplified using primers (AAQ47843-70). Related single specific primers using a gene sequence coding for the haem-binding region of cytochrome P450 are shown in (AAQ4781-Q47903). (Updated on 25-MAR-2003 to correct PN field.) (Updated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        petunia, tobacco and carnation, using a suitable vector such as agrobacterium, give transformed plants which express the gene, resulting
                                                          Gene coding for flavonoid-3',5'-hydroxylase of petunia petals - used to transform plants e.g. petunia, rose or tobacco to give bluer flower colour and altered pigment pattern.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSP for flavonoid-3',5'-hydroxylase gene product.
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 33; DB 2;
Pred. No. 3.9e+02;
5; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                              24-OCT-2003 to standardise OS field)
                                                                                                                                            Claim 11; Page 59; 82pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11; Page 55; 82pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR40870 standard; protein; 11 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
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FGGGPRKCVG 11
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  WPI; 1993-303469/38.
N-PSDB; AAQ47881.
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Best Local Similarity
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28-MAR-1994
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AAR40870;

RESULT 30

셤 8

AAR4087

Matches

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Gaps

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- used

petals - used bluer flower

Kikuchi

Shimada R;

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petunia, tobacco and carnation, using a suitable vector such as agrobacteratium, give transformed plants which express the gene, resulting in petals with a bluer colour than normal, and/or pigmentation patterns which do not occur naturally. The sequences were amplified using primers shady and a single specific primers using a gene sequence coding for the haem-binding region of cytcohrome P450 are shown in (AAQ47871-Q47903). (Updated on 25-MAR-2003 to correct PN field.) (Updated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plant; aspen; phenylpropanoid pathway; agronomic; lignin; paper; 4-coumarate-CoA ligase; 4CL; coniferyl aldehyde 5-hydroxylase; CAld5H; S-adenosyl-I-methionine-dependent; 5MM; AldOMT: transgenic; grass; 5-hydroxyconiferaldehyde O-methyltransferase; cellulose; pulp; coniferyl alcohol dehydrogenase; CAD; sinapyl alcohol dehydrogenase; SAD; syringyl; guaiacyl; agriculture; haem-binding domain; P450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene coding for flavonoid-3',5'-hydroxylase of petunia petals - used to transform plants e.g. petunia, rose or tobacco to give bluer flower
                                                                                                       Flavonoid-3',5'-hydoxylase; transformation; plants; petunia; rose; tobacco; pigment alteration; blue; SSP; single specific primer; PCR; polymerase chain reaction; amplification; expression; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                      Ohbayashi M, Shimada R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 33; DB 2; Length 11; 40.0%; Pred. No. 3.9e+02; tive 6; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conserved haem-binding domain of P450 proteins.
                                                                       SSP for flavonoid-3',5'-hydroxylase gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                        Shimada Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transform plants e.g. petunia, rose
colour and altered pigment pattern
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                                       (first entry)
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2 FGAGRRVCPG 11
(revised)
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N-PSDB; AAQ47876.
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                                                                                                                                                                                             Petunia x hybrida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11 AA;
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24-OCT-2003
25-MAR-2003
28-MAR-1994
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Okinaka Y;
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Best Local &
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene coding for flavonoid-3',5'-hydroxylase of petunia petals - usectransform plants e.g. petunia, rose or tobacco to give bluer flower colour and altered pigment pattern.
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Pred. No. 3.9e+02;
6; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                SSP for flavonoid-3',5'-hydroxylase gene product.
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                                                                                                                                                           AAR41635 standard; protein; 11 AA
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(revised)
(first entry)
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Okinaka Y;
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FGAGRRICPG 11
                         FXXGXXXCXG
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Best Local Similarity
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25-MAR-2003
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Gaps

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Synthetic

AAR40875;

RESULT 33

AAR40875

Matches

ઠે 셤 Pepper; cytochrome P450; PepCYP; incompatible interaction.

associated peptide

Pepper cytochrome P450 (pepCYP)

(first entry)

15-JUL-2004

ADO58606;

ADO58606 standard, peptide, 11 AA

RESULT 35

/note= "All.Xaa residues are unknown"

Location/Qualifiers

Misc-difference 1.

Unidentified

KR2001081198-A

29-AUG-2001

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The invention relates to a method of genetically transforming a plant simultaneously with multiple genes from the phenylpropanoid pathways, comprising incorporating into the genome of the plant, a number of genes, their substantially similar fragments or their combinations, to produce plants displaying alered agronomic traits. The genes are selected from commarate-CoA ligase (4CL), coniferyl aldehyde 5-hydroxylase (CAld5H), sedenosyl-L-methionine (SAM), dependent 5-hydroxyconiferaldehyde 0-methyltransferase (Ald6MT), coniferyl alcohol dehydrogenase (CAD) and sinapyl alcohol dehydrogenase (SAD). The method is useful for the composition of plant tissue for the alteration of lighin monomer composition, increased syringyl/guaiacyl (S/G) lighin ratio and increased cellulose content and transgenic plants resulting from such transformations. This is an improved method to simultaneously control the lighin quantity, lighin compositions, and cellulose contents in plants, and is applicable to all plant species that are susceptible to the transfer of genetic information by Agrobacterium or other gene delivery system. The method is of particular value to paper and pulp industries because lighin containing higher syringyl monomer content is more susceptible to chemical delighification. Woody plants transformed with the constructs offer a signification. Woody plants transformed with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     potential economic benefit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genetically transforming plant with multiple genes from phenylpropanoid pathways, comprises incorporating number of genes into the genome of the plant, to produce plants displaying altered agronomic traits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   process over conventional paper feedstocks. Similarly, modification of the lignin composition in grasses by insertion and expression of heterologous SAD gene offers a unique method for increasing the digestibility of grasses and is of significant potential economic benefit to the farm and agricultural industries. The present sequence represents the amino acid sequence of the conserved has—binding domain of P450 proteins, which has homology to CAldSH as described in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UNMT ) UNIV MICHIGAN TECHNOLOGICAL,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure, Page 6, 95pp, English.
                                                                                'label= unknown
                                                                                                                                                                 label= unknown
                                                                                                                                                                                                                                                           'label= unknown
                                                                                                                                                                                                                                                                                                                                       label= unknown
                                                                                                                                                                                                                                                                                                                                                                                                                        /label= unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-SEP-2001; 2001WO-US027445.
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Best Local Similarity
.-hes 9; Conserv?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-351773/38.
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                                   Misc-difference
                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                         Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-MAR-2002
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Pepper cytochrom p450 gene(pepcyp) highly expressed during incompatible interaction between colletotrichum gloeosporioides and peppers.

Disclosure; Page 2; 16pp; Korean.

(KOKU-) KOREA KUMHO PETROCHEMICAL CO LID

oh BJ;

Ko MG,

Kim YS,

WPI; 2002-128887/17.

11-FEB-2000; 2000KR-00006345.

11-FEB-2000; 2000KR-00006345.

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                                                                                                                                                                                                                                                                                                                                     The present invention relates to the isolation of a pepper (Capsicum annum) cytochrome P450 gene (PepCYP), which is highly expressed by incompatible interaction between Colletotrichum gloeosporioides and peppers. The present peptide sequence of unknown function is given in the specification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tobacco; plant; cytochrome P450; disease resistance; biosynthesis; lipid; hormone; insect attractant; secondary metabolite; herbicide; pesticide; pollutant; deterrent; insect predator; flavouring; antibacterial; fungicide; virucide; insecticide.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 33; DB 5; Length 11;
Pred. No. 3.9e+02;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytochrome P450 protein conserved domain #3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE30014 standard, peptide, 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                      100.001
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                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 80.0 Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 FXXGXXXCXG 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
Misc-difference 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nicotiana tabacum.
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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AAE30014
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Score 33; DB 5; Length 11; Pred. No. 3.9e+02; ; Mismatches 0; Indels.

100.0%; 90.0%; E

Conservative 1 FXXGXXXCXG 10 FGXGXXXCXG 11

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The consensus sequence of haem-binding domains for microsomal cytochrome P450 homologues was used to design synthetic PCR prinners. The primers may be used in PCR for amplification of peral cytochrome P450 homologues. See also AAR30868-75. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                Nucleic acid sequence encoding a di.hydro:kaempferol-hydroxylating enzyme - e.g. cytochrome P450 introduced into transgenic plants for controlling flavonoid pigmentation in plants and organisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention provides new DNA molecules (AAX60773-X60781) encoding soybean cytochrome P450 enzymes (AAY09183-Y09191) respectively. The Iencoding the cytochrome P450 enzymes is useful for transformation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Soybean, Solanaceae crop plant, cytochrome P450; transgenic plant, enzyme; phenylurea herbicide, herbicide resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Soybean cytochrome P450 enzyme conserved peptide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                              Lester
                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 33; DB 2;
Pred. No. 4.5e+02;
4; Mismatches 0;
                                                                                                                            Kovacic F, Tanaka Y,

    .13
/note= "Xaa is any amino acid"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding soybean cytochrome P450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                              Disclosure, Page 13; 66pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2; Page 26; 93pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY09192 standard; peptide; 13 AA.
                                                                                         (ITFL-) INT FLOWER DEV PTY LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                   91AU-00007173.
92AU-00000923.
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92EP-00306379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conservative
                                                                                                                              Cornish EC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dewey RE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |::||:||:|
FGAGXRXCLG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 FXXGXXXCXG 10
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                                                                                                                                                                   WPI; 1993-010688/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference 1.
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 13 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-OCT-1997;
10-JUL-1992;
                                   11-JUL-1991;
                                                      17-FEB-1992;
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                                                                                                                              Holton TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY09192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a new isolated cytochrome P450 polypeptide. The invention is useful for conferring disease resistance on a plant or plant component. Occamponent conferring disease resistance on a plant or plant component. The cytochrome p450 polypeptide is useful in the biosynthesis of hormones, lipids, and secondary metabolites, and may also help plants tolerate potentially harmful exogenous chemicals such as herbicides, pesticides and pollutants. In addition, the polypeptide is useful in the chemical defense of the plants against insects, as well as against bacterial, viral, or fungal infection. The polypeptide may also be used in the production of insect attractants and deterrents, which may also deter insect pests or attract insect predators, and in generating flavourings. The present sequence is Nicotiana tabacum cytochrome P450 protein conserved domain
                                                                                                                                                                                                                                                                                                                                                                                           New cytochrome P450 polypeptide useful for the biosynthesis of hormones, lipids and secondary metabolites, and in increasing the resistance of plants against harmful exogenous chemicals, e.g. herbicides, pesticides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 33; DB 6; Length 11;
Pred. No. 3.9e+02;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Consensus haem-binding domain of microsomal cyt-P450.
                                                                         /note= "Xaa can be any amino acid"
                     /note⇒ "Xaa can be any amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR30868 standard; protein; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure, Fig 4A; 78pp; English.
                                                                                                                                                                                                                                                                                (KENT ) UNIV KENTUCKY RES FOUND.
   /label= Unknown
                                                      label= Unknown
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                                                                                                                                                                                                                         09-MAR-2001; 2001US-0274421P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
                                                                                                                                                                                                                                                                                                                       Ralston LF;
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FGXGRRXCPG 11
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                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-018735/01.
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Best Local Similarity
                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11 AA;
                                                                                                            WO200272758-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                 or pollutants
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12-MAY-1993
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Gaps

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DNA

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Gaps

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Indels

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Mismatches

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Conservative

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Matches

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Solanaceae crop plants. Transgenic plants comprising DNA constructs having the P450 encoding nucleic acid sequences are resistant to phenylurea herbicides. The transgenic plants have increased resistance to phenylurea herbicides compared to wild-type plants of the same species. The plant crops, e.g. turfgrass, tobacco, potato, tomato, corn, rice, cotton, soybean, rape, wheat, oats, barley or rice are particularly resistant to fluometuron, linuron, chlortoluron or diuron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cancer treatment, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid encoding flavone synthase II, useful e.g. for producing transgenic plants with altered flower color or flavone content.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            synthage II (FNSII) which has anticancer and immunocodulatory activity. FNSII catalyses conversion of naringenin to apigenin. (I) is used to produce transgenic ornamental plants that have targeted alterations in flower color, also altered content/distribution of flavones in leaves, flowers and other tissues, e.g. increased resistance properties or symblotic capacity. FNSII expressed by (I) is used in synthesis of flavones that are useful as pharmaceuticals, e.g. in cancer treatment, or as biologically active substances, e.g. to improve the immune defence system. Objequuelocited fragments of (I) are used as probes and primers, or as antisense or ribozyme agents for regulating expression of (II). (Updated on 12-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gerbera, transgenic plant; flavone synthase II; FNSII; anticancer;
immunomodulator; naringenin; apigenin; ornamental plant; flower colour;
pharmaceutical; cancer; treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes a novel nucleic acid (I) that encodes flavone
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                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                100.0%; Score 33; DB 2; Length 13; 80.0%; Pred. No. 4.5e+02; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB11394 standard; protein; 13 AA.
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                                                                                                                                                                                                                                                                                                                                            99DE-01018365
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 FXXGXXXCXC 10
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(FORK/) FORKMANN G.
                                                                                                                                                                                                                                                                                    Sequence 13 AA;
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22-FEB-2001
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Best Local S
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Matches
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LID AAB.
LID AAB.
LID AAB.
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100.0%; Score 33; DB 3; Length 13; 70.0%; Pred. No. 4.5e+02;

Best Local Similarity

Query Match

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The invention relates to nucleic acids (AAH79386-AAH80036) encoding polymorphic variants of proteins (AAG98010-AAG98238) related to polymorphic variants of proteins (AAG98010-AAG98238) related to angiopolatin, 4-hydroxybutyrate, dehydrogenses, adenosine triphosphate (ATP)-dependent RNA helicase, major histocompatibility complex (MHC) class I histocompatibility antigen and/or phosphoglycerate kinase. These cucles and single nucleotide polymorphisms (SNR9) and the encoded proteins have potential immunosuppressive, immunostimulatory, critical antirheumatic, antisclerotic, antidiabetic, antinflammatory, cytostatic, antirheumatic, antisclerotic, antidiabetic, antinflammatory, cytostatic, antirheumatic, antisclerotic, antidiabetic, antinflammatory, cuseful in gene/protective and antimicrobial activity and may be useful in gene/protein therapy, vaccines, modulation of the expression and activity of proteins related to angiopoietin, 4-hydroxybutyrate, chistocompatibility complex (MHC) Class I histocompatibility antigen chistocompatibility complex (MHC) Class I histocompatibility antigen and/or phosphoglycerate kinase. Disorders that may be prevented, cliseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus creather brain, breast, colon and kidney, leukemia), diseases of the nervous system, an infection of pathogenic organisms. They may also be conserved and chairsances and craw as longevity, appearance, strength,
                                                                                                                                                                                                                                                                                                                                                                                                                 phosphoglycerate kinase; immunosuppressive; immunostimulatory; antirheumatic; antisclerotic; antidiabetic; antiinflammatory; cytostatic; antileukemic; neuroprotective; antimicrobial; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                               major histocompatibility complex Class I histocompatibility antigen; MHC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polymorphic nucleic acids encoding e.g. angiopoietin, dehydrogenase, adenosine triphosphate-dependent RNA helicase and/or phosphoglycerate kinase, useful for diagnosing and treating, e.g. cancer, autoimmune
                                                                                                                                                                                                                                                                                                                               Human; single nucleotide polymorphism; SNP; angiopoietin;
                                                                                                                                                                                                                                                                                                                                                 4-hydroxybutyrate; dehydrogenase; protein therapy; adenosine triphosphate-dependent RNA helicase;
                                                                                                                                                                                                                                                                                      Human SNP associated peptide SEQ ID NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 461; 484pp; English.
                                                                                                                                                    AAG98132 standard; peptide; 14 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-DEC-2000; 2000WO-US035346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-00472688
                                                                                                                                                                                                                                          19-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diseases and infections
1 PXXGXXXCXG 10
                      |:||:||||
FGXGRRXCXG 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leach M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-418297/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200148245-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shimkets RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   speed and
                                                                                                                                                                                                 AAG98132;
                                                                                                           RESULT
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RESULT 41

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AAP20076

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The inventors claim a vaccine against HBV which comprises one of AAP50146-P50151 together with one of AAP50152-P50156 and a diluent. They also claim a vaccine which comprises a synthetic polypeptide having an AA residue sequence immunologically corresp. to portions of a sequence of the virus surface antigen (a) from posns. 38-52, and (b) from posns. 110-137, from the aminot terminus, together with a diluent. Other portions of sequences may be similarly used, (see AAP50158, AAP50160, AAP50162). (Updated on 16-AUG-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis B virus; surface antigen; antibody; radiolabel; enzyme; label;
disease diagnosis; ss.
                          Sequence of synthetic peptide used in vaccine against hepatitis B virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Labeled synthetic peptide used to recognise hepatitis B virus surface
                                                                                                                                                                                                                                                                                                                                                                           - useful in vaccines against hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 33; DB 1;
Pred. No. 5.1e+02;
6; Mismatches 0
                                                                           Vaccine; immunogen; antigen; epitope; diagnosis.
                                                                                                                                                                                                                                                                                   (SCRI ) SCRIPPS CLINIC & RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAP60758 standard; protein; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                           Claim la; Page 61; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                             New synthetic polypeptide(s) - 1 virus and for diagnostic tests.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82US-00426309.
                                                                                                                                                                                                        85EP-00301588
                                                                                                                                                                                                                                                    84US-00588122
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Best Local Similarity 40.0%;
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (revised)
(first entry)
07-OCT-1991 (first entry)
                                                                                                                                                                                                                                                                                                                 Chisari FV;
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4 FLGGTTVCLG 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antigen or antibody
                                                                                                           Hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 15 AA;
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                                                                                                                                                                                                        07-MAR-1985;
                                                                                                                                                                                                                                       39-MAR-1984;
                                                                                                                                                                                                                                                    09-MAR-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-MAR-2003
01-JAN-1980
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                                                                                                                                                                         18-SEP-1985
                                                                                                                                                                                                                                                                                                                  Milich DR,
                                                                                                                                          EP155146-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
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                                               (HBV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The peptide is a synthetic peptide specific antigenic determinant region, it is synthesised based on the sequence of a specific antigenic determinant of a desired natural genome. It can be used in the prodn. of antigens which can be used to produce vaccines, diagnostic or therapeutic antibodies etc. The antigens produced are highly specific and free of undesirable impurities. See also AAP20068-P20094. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic specific antigenic determinants - comprising peptides with amino acid sequence determined from gene DNA sequence.
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No. 5.18+02; Indels
                                                                                                                                                                                                                                                                                       Synthetic peptide specific antigenic determinant region i.
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 Score 33; DB 4; Length 14;
Pred. No. 4.8e+02;
6; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                    Antigen; vaccine; diagnostic; therapeutic antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lerner RA, Green N, Sutcliffe JG, Shinnick TM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 5.1e
6; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAP50146 standard; peptide; 15 AA.
                                                                                                                                                                           AAP20076 standard; protein; 15 AA.
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 100.08;
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81US-00248059.
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                   40.08;
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(first entry)
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                                4; Conservative
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FLGGWWVCLG 13
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                                                                                   |::|::|:|
2 FHYGVLACEG
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   Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                17-JUL-1980;
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27-MAR-1981;
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01-DEC-1992
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16-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                     Synthetic.
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Matches

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AAP50146

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Gaps

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Sequence 15 AA
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                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                  RESULT 45
                                                                                                                                                                                                                                                                            AAR82090
ID AAR8
  88888888888888888888888888
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                                                                                                                                                                                                                                                                                                                                                                                                                                      T helper determinant in the S region of HBsAg from amino acid
                                                                                                                             This radio-labeled or enzyme-labeled peptide is used in the detection of hepatitis B virus surface antigen or antibody. The method involves contacting the sample with the labeled peptide which is normally recognized and bound by the antibody suspected of being present in the sample. The contacted sample is incubated and washed. Staphylococi brotein-A are then added to the contacted sample with the resultant mass being incubated and centrifuged. The radioactivity or enzymatic activity of the resultant pelleted bacteria is then determined. See also AAP60750-7, AAP60759-61. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vaccines comprising anti-idiotype antibody conjugates - induce prodn. of neutralising antibodies against HIV-1 for immunisation against HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention includes epitope-directed immunization with a vaccine in which an anti-idiotype antibody is conjugated to a carrier, which can be either a protein or its derived T helper peptide. The carrier is one
                                                                         Detection of Hepatitis B surface antigen or antibody - using labelled synthetic peptide.
                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                        Length 15;
                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                       Score 33; DB 1;
Pred. No. 5.1e+02;
5; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 9; Page 25 and page 16-17; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vaccine; AIDS; HIV-1; carrier peptide.
                                                                                                                                                                                                                                                                                                                                                                   AAR24422 standard; peptide; 15 AA.
                  (NYBL-) NEW YORK BLOOD CENTER INC
                                                                                                            Claim 7; Page 23; 15pp; English
                                                                                                                                                                                                                                                       100.0%;
 82US-00426309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90US-00616247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91WO-US008653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TANO-) TANOX BIOSYSTEMS INC
                                                                                                                                                                                                                                                                                                                                                                                                          (revised)
(first entry)
                                                                                                                                                                                                                                                                           4; Conservative
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                                                                                                                                                                                                                                                                                                                 4 FLGGTTVCLG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                 residue numbers 38-52
                                                                                                                                                                                                                                                                                               1 FXXGXXXCXG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fung MSC;
                                                          WPI; 1986-155507/24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1992-199955/24.
                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neutralising antibo
infection and AIDS.
                                                                                                                                                                                                                                   Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9208491-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-NOV-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                         25-MAR-2003
21-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence of
                                      Neurath AR;
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                                                                                                                                                                                                                                                                                                                                                                                      AAR24422;
                                                                                                                                                                                                                                                                           Matches
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against which the vaccine recipient has previously immunized or otherwise previously exposed, or which enhances the immune response against the anti-idiotype antibody. One exemplary anti-idiotype antibody which induces antibodies against the PND is AB19-4. Where the anti-idiotype induces antibodies against the PND is AB19-4. Where the anti-idiotype or a peptide of either HBsAg or HIV-1 p24 including a T helper or a peptide of either HBsAg or HIV-1 p24 including a T helper or determinant. "PND" = the principal neutralizing determinant ("PND") of spl20. It is known that many individuals in the high risk groups for HIV-1 infection are also at high risk for hepatitis B virus infection. Many people in these groups have already been vaccinated with the hepatitis B virus vaccine using hepatitis B surface antigen (HBsAg). Thus, HBsAg (and related T helper peptides) is a preferred carrier for conjugation with an anti-idiotype antibody which induces production of HIV-1 neutralizing antibodies. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic peptide T cell epitope analogue (retro-)inverso modified - conjugated with a B cell epitope in a vaccine tailored to a specific condition, e.g. polio, hepatitis B, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Retro-inverso modified, T cell epitope, analogue, vaccine, B cell; immunisation; HBV; major surface antigen; residues 38-52.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis B virus major surface antigen 38-52 T cell epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 33; DB 2;
Pred. No. 5.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
40.0%; E
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FLGGTTVCLG 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tyler MI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1995-311503/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9523166-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAR-2003
03-APR-1996
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DB 2; Length 15;

100.0%; Score 33;

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AAU91319 standard; peptide; 15

(first entry)

18-JUN-2002

AAU91319;

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The present sequence represents an immunogenic peptide, derived from the S antigen, which is useful for generating antigen specific T cells. It may be used in the course of the invention. The specification describes the use of an agent which regulates cell proliferation for modulating the levels of production of a gene product of interest in a host organism. The method comprises transforming an expandable population of cells with a transgene encoding the gene product, expressing the gene in the host and regulating proliferation of the population of cells by administration of the agent. The method is useful for regulating cell proliferation. The method is also useful for delivering one or more transgenes useful in the disorder, neurodegenerative disorder, atherosclerosis, rheumatological arthritis, osteoporosis, chronic ulcers, psoriasis, raeumatoid arthritis, osteoporosis, directious diseases
                  ö
                                                                                                                                                                                                                                                                                                                   Immunogenic peptide; antigen specific T cell; cell proliferation; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Regulating expression of transgenes encoding enzymes or hormones in mammals, by transforming expandable population of cells with desired transgene and regulating cell proliferation by administration of an
                    Gaps
                                                                                                                                                                                                                                                                                  Immunogenic peptide useful for generating antigen specific T cells
                                                                                                                                                                                                                                                                                                                                    inflammation; autoimmune disease; dermatological disorder;
neurodegenerative disorder; atherosclerosis; rheumatoid arthritis;
osteoporosis; chronic ulcer; psoriasis; cardiovascular disease;
                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 33; DB 3; Length 15; 40.0%; Pred. No. 5.1e+02; ive 6; Mismatches 0; Indels
                    0; Indels
   Pred. No. 5.1e+02;
                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure, Page 22; 37pp; English
                                                                                                                                                                               AAB19305 standard; peptide; 15 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAR-1999; 99GB-00007366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAR-2000; 2000WO-GB001225
40.04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MEDI-) MEDICAL RES COUNCIL.
                                                                                                                                                                                                                                                     (first entry)
                       Conservative
                                                       FXXGXXXCXG 10
                                                                                        4 FLGGTTVCLG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-647208/62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
 Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                               infectious disease
                                                                                                                                                                                                                                                                                                                                                                                                                                Hepatitis A virus.
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                                                                                                                                                                                                                                                   19-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fisher A;
                                                                                                                                                                                                                  AAB19305;
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The invention relates to an isolated human cytochrome P450TEC (thywns expressed cytochrome) polypeptide or the encoded sequence included in expressed cytochrome) polypeptide or the encoded sequence included in expressed cytochrome) polypeptide or the polymucleotide encoding P450TEC acid can modulate, complement, or species homologue, where the muclaic acid can modulate, or encodes a peptide that modulates care the muclaic acid metabolism and hydroxylation of arachidonic acid metabolism and hydroxylation of arachidonic acid encodes a peptide that modulates can acidity in a biological assay or condition related to P450TEC and for identifying an activity in a biological assay, by expressing cativity in a biological assay and identifying the protein in the activity in a biological assay and identifying the protein in the cypernatant having the activity. The nucleic acid is useful for disease or inflammatory response of a patient or a predisposition to the disease cor inflammatory response of a patient or a predisposition to the disease by detecting a polymorphism in P450TEC gene. P450TEC antibody is cuseful for quantifying the level of P450TEC in a sample and for treating disease or condition related to P450TEC. P450TEC polymucleotides or identifying the level of P450TEC or in sample and for treating cuseful for quantifying the level of P450TEC in a sample and for treating disease or condition related to P450TEC. P450TEC polymucleotides or cyplypeptides are useful as marker or detector of a particular immune system disease or disorder and in treating or detecting autoimmune cypseem disease or disorder and in treating or detecting autoimmune cypseem disease or disorder and in treating or detecting autoimmune cypseem disease and organs. C Goodpasture's Syndrome, Grave's disease, multiple solerosis, myasthenia crejection or graft versus-host disease. Pa60TEC in tomitor program crejection or graft versus-host disease. Sundrome, disease states involving P450TEC or to manitor programs or trierapy. P450TEC attagonistes ar
                                                                                                                                                               Thymus expressed cytochrome; arachidonic acid metabolism; autoimmune disorder; Addison's disease; haemolytic anaemia; rheumatoid arthritis; dermatitis; allergic encephalomyelitis; glomerulomaphritis; Goodpasture's Syndrome; Grave's disease; multiple sclerosis; myasthenia gravis; neuritis; organ rejection; systemic lupus erythematosus; insulin dependent diabetes mellitus; autoimmune inflammatory eye disease; graft versus-host disease; inflammatory disease; infection; septics block; sepsis; SIRS; systemic inflammatory response syndrome; ischaemia reperfusion injury; arthritis; inflammatory bowel disease; Crohn's disease; thymoma; P450TEC; immune system disease; haeme binding motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human cytochrome P450TEC, thymus expressed cytochrome polypeptides for diagnosing, treating autoimmune disorders e.g. Addison's disease, dermatitis, rheumatoid arthritis and identifying modulators.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  White JA, Ramshaw HA, Stangle WA;
                                                                                                                            Cytochrome P450 haeme binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 65; 154pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-APR-2001; 2001WO-CA000547.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-APR-2000; 2000US-0198617P. 01-JUN-2000; 2000US-0208785P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jones G, Petkovich PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CYTO-) CYTOCHROMA INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-291654/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200181585-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unidentified
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Gaps

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4; Conservative

Best Loc Matches

1 FXXGXXXCXG 10 |::|:::|:|
FLGGTTVCLG 13

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           including inflammation associated with
and chronic inflammatory diseases, including inflammation associated wit infection (e.g. septic shock, sepsis, systemic inflammatory response syndrome (SIRS)), ischaemia reperfusion injury, arthritis, inflammatory bowel disease, Crohn's disease and conditions of the thymus, such as thymomas. The present sequence is a cytochrome haeme binding motif used in sequence similarity searches to identify nucleic acid sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention relates to an isolated polynucleotide encoding a cytochrome P450 polypeptide which when expressed in a plant produces at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotides encoding a cytochrome P450 polypeptide, useful for producing plants with enlarged or parthenocarpic fruits, in increasing plant tissue size to increase agricultural yields, or producing male-
                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis, cytochrome P450, cP450, plant, parthenocarpic, fruit, enlarged fruit, transgenic, vegetable size, grain size, soybean, leaf size, flower size, agricultural yield, male-sterile plant,
                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana cytochrome P450 protein peptide fragment #5.
                                                                                                                                                                               ö
                                                                                                                                                   Length 15;
                                                                                                                                                100.0%; Score 33; DB 5; Length 15
100.0%; Pred. No. 5.1e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Val, Ile, Ala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                      ABG75617 standard; peptide; 15 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure, Page 3; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= Ala, Ser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fromm M, Meyerowitz E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-00349385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0115967P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'label= Arg,
                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                            10; Conservative
                                                                                                                                                                                                        1 PXXGXXXCXG 10
                                                                                                                                                                                                                                    FXXGXXXCXG 11
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(FROM/) FROMM M.
(MEYE/) MEYEROWITZ E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-198390/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 orchid; maize.
                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Phalaenopsis sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JS2002152495-A1.
                                                                                                                      Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sterile plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pinus radiata.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                               16-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycine max.
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                                                                                                                                                Query Match
Best Local Si
Matches 10,
                                                                                                                                                                                                                                                                                                                                  ABG75617;
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                                                                                                                                                                                                                                                                             RESULT 48
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fruit. The invention also discloses a recombinant construct comprising the novel polynucleotide which when expressed in a plant produces a plant with a parthenocarpic fruit or enlarged fruit. Also disclosed is a isolated polynucleotide encoding a cytochrome P450 or comprising an isolated polynucleotide encoding a cytochrome P450 polypeptide which when expressed in a plant produces a plant with a parthenocarpic fruit or enlarged fruit compared with a plant packing the isolated polynucleotide. The cytochrome P450 polypeptide and polynucleotide of the invention is useful in the production of plants with seedless, enlarged, or parthenocarpic fruits, including vegetable or grain size, leaf size or parthenocarpic fruits, including vegetable or grain size, leaf size or size. The sequences may also be used in increasing plant tissue size to increase agricultural yields of plants, to produce male-sterile plants and to screen for compounds that control parthenocarpy or fruit that the control parthenocarpy or fruit that and to screen for compounds that control parthenocarpy or fruit that the control part that control parthenocarpy or fruit that the control pa
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                                                                                                                                                                                                                                                                                                                                                                                                       size in plants. The present sequence represents a cytochrome P450 peptide of the invention, this sequence is highly conserved in cytochrome P450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Use of at least one set of peptides in the preparation of a medicament for modulating an immune response, and for treating cancer or yeast, viral, bacterial, protozoal and mycoplasma infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vaccine, virucide, antigen, autoimmune disease, infection, inmune modulation, cancer, neoplasm, cytostatic; melanoma, lung tumor; breast tumor; uterine cervix tumor; prostatic cancer, colon tumor; pancreas tumor; stomach tumor; bladder tumor; kidney tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
   east one phenotype selected from parthenocarpic fruit and enlarged
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 33; DB 6; Length 15; Pred. No. 5.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADV23624 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
70.0%; P
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25-MAR-2004; 2004AU-00901589.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-MAR-2005 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Conservative
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FGXGXRXCPG 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 15 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proteins
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WPI; 2005-031657/03

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concluded are an antigen-presenting cell which has been contacted with the included are an antigen-presenting cell which has been contacted with the peptides above and thus presents the peptides, a population of such antigen-presenting cells, a process for producing antigen-presenting cells, a process for producing antigen-presenting cells, a process for producing antigen-presenting cells a process for producing antigen-presenting comprising antigen-specific lymphocytes, a composition computing antigen-specific lymphocytes, a composition computing antigen-specific lymphocytes, a composition of comprising antigen-specific lymphocytes, a composition of comprising antigen-specific lymphocytes, and properties of interest comprising administering to a patient in need at least one set of the peptides, a method for treatment and/or prophylaxis of a disease or condition-associated with the presence of a polypeptide of interest a subject to a target antigen. The polypeptide that is a polypeptide of interest composition of matter for modulating an immune response in a subject to a target antigen. The polypeptide that is a polypeptide of produced by a pathogenic organism or a cancer, and produced by a pathogenic organism or a cancer, and produced by a pathogenic organism or a cancer, in a produced by a pathogenic organism or a cancer, polypeptide is produced by a cancer selected from melanoma, lung cancer, protocomed by a pathogenic cancer, prostate cancer, condition-associated composition and mycoplasmas. The disease, or condition-associated cancer, cervical cancer, prostate cancer, post transplant in protocomer, stomach cancer, prostate cancer, kidney cancer, post transplant antigen-presenting cells or their present for the treatment of a disease or condition is associated with the presence or aberrant expression of a target antigen, where the antigen presenting cells or their present antigen to express a processed or moditions but have been contacted with an antigen that corresponds to the target antigen to express a p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              virus protein
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Gaps
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Score 33; DB 9; Length 15; Pred. No. 5.1e+02; 6; Mismatches 0; Indels
                          9
   100.08;
            40.04;
                          Conservative
                                                  1 FXXGXXXCXG 10
 Query Match
Best Local Similarity
                           Matches
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|::|:::|:: 2 FLGGTTVCLG 11

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ADV23625 standard; peptide; 15 AA.
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RESULT 50
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ADV2

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YACC

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YACC

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YACC

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YACC

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Vaccine; virucide; antigen; autoimmune disease; infection; immune modulation; cancer; neoplasm; cytostatic; melanoma; lung tun breast tumor; uterine cervix tumor; prostatic cancer; colon tumor; pancreas tumor; stomed tumor; bladder tumor; kidney tumor; hodgkin's lymphoma

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Hepatitis B virus
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WO2004108753-A1.

10-JUN-2003; 2003AU-00902875. 25-MAR-2004; 2004AU-00901589. 10-JUN-2004; 2004WO-AU000775. 16-DEC-2004.

UYME ) UNIV MELBOURNE Kent SJ;

The invention relates to the use of at least one set of peptides in the preparation of a medicament for modulating an immune response, where individual peptides of a respective set comprise different portions of a mino acid sequence corresponding to a single polypeptide of interest and display partial sequence identity or similarity to at least one other comprise of the same set of peptides (i.e. they are overlapping). Also peptide of the same set of peptides (i.e. they are overlapping). Also cincluded are an antigen-presenting cell which has been contacted with the peptides above and thus presents the peptides, a population of such antigen-presenting cells, a process for producing antigen-presenting cells, a process for producing antigen-presenting cells, a method for modulating an immune response to a polypeptide of interest, a method for modulating an immune response to a polypeptide of interest comprising administering to a patient in need at least one set of the peptides (and a carrier and/or composition) a method for modulating an immune response to a polypeptide of interest contaction associated with the presence of a polypeptide of interest or condition associated with the presence of a polypeptide of interest cand a composition of matter for modulating an immune response in a subject to a target antigen. The polypeptide that is a polypeptide condition-associated polypeptide that is a polypeptide by a pathogenic organism or a cancer, and produced by a pathogenic organism or a cancer, or condition-associated from yeast, viruses, bacteria, helminths, produced by a pathogenic organism or a cancer, colon cancer, post transplant color cancer, stomach cancer, bladder cancer, colon cancer, post transplant color presenting cells or their precureors are useful in the proplem or a medicament for the treatment of a disease or condition is associated with the presenting or a particular presenting or condition is associated where the antigen-presenting of a tarder antigen. Where the antigen-presenting of a tarder an or aberrant expression of a target antigen, where the antigen-presenting cells or their precursors have not been subjected to activating conditions but have been contacted with an antigen that corresponds to the target antigen to express a processed or modified form of the antigen for presentation to the subject's immune system. The present sequence is one of a set of overlapping immunogenic peptides derived from a Hepatitis Use of at least one set of peptides in the preparation of a medicame for modulating an immune response, and for treating cancer or yeast, viral, bacterial, protozoal and mycoplasma infections. invention relates to the use of at least one set of peptides in Disclosure; SEQ ID NO 2045; 645pp; English. B virus protein. 

; Score 33; DB 9; Length 15; Pred. No. 5.1e+02; 6; Mismatches 0; Indels 100.0%; 40.04; 4; Conservative Best Local Similarity Sequence 15 AA; Query Match Matches

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8, 2006, 11:19:58 Search completed: March Job time : 194 secs us-10-751-235-14.dx.rapbn

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502, App
1228, Ap
458, App
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18243, A
12, Appl
7405, Ap
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464, App
15685, A
99, Appl
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US-11-087-099-2635
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US-11-087-099-8664
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US-11-234-786-114
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Sequence 25378, A Sequence 10778, A Sequence 10778, A Sequence 542, App Sequence 546, App Sequence 494, App Sequence 548, App
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Sequence 25, Appl
Sequence 43, Appl
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1478, Ap
6613, Ap
464, App
460, App
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15, Appl
500, App
516, App
540, App
68, Appl
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8: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_FUB.pep:*
            GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-11-205-109-25

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US-11-006-566A-25378

US-11-116-881A-542

US-11-116-881A-546

US-10-467-657-8472

US-10-467-657-8472

US-10-467-657-8472

US-11-116-881A-549

US-11-116-881A-2299

US-11-1072-512-3124

US-11-1072-512-3124

US-11-1087-099-6613

US-11-1087-099-6613

US-11-116-881A-460

US-11-116-881A-460

US-11-116-609-14

US-11-116-609-14

US-11-16-609-15

US-11-116-881A-500

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Maximum Match 100%
Listing first 100 summaries
                                                               protein search, using sw model
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Maximum DB seq length: 200000000
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Query Match
Best Local Similarity 40.0
Matches 4; Conservative
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21 FGAGPRNCLG 30
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1 FOAGPRICLG 10
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Matches 4; Conserval
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ORGANISM: bacteria
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Sequence 20853, A
Sequence 34393, A
                                                                                                                                                                                                                      APPLICANT: ALBERTSEN, MARC C.
APPLICANT: ALBERTSEN, MARC C.
APPLICANT: FOX TIM
APPLICANT: HUFWAN, GARY
APPLICANT: HUFWAN, GARY
APPLICANT: TRIMMELL, MARY
TITLE OF INVENTION: NUCLECTIDE SEQUENCES MEDIATING MALE FERTILITY AND
TITLE OF INVENTION: METHOD OF USING SAME
FILE REFERENCE: 1146R
CURRENT FILING DATE: 2005-06-24
CURRENT FILING DATE: 2003-04-11
PRIOR FILING DATE: 2003-04-11
PRIOR FILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 34
SEQ ID NO 24
LENGTH: 10

LENGTH: 10

LENGTH: 10
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Publication No. US20060015968A1
GENERAL INFORMATION:
APPLICANT: ALBERTEN, MARC C.
APPLICANT: FOX, TIM
APPLICANT: FOX, TIM
APPLICANT: TRIMPELL, MARY
APPLICANT: TRIMPELL, MARY
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES MEDIATING MALE FERTILITY AND
TITLE OF INVENTION: METHOD OF USING SAME
FILE REFERENCE: 1148CR
CURRENT APPLICATION NUMBER: US/11/166,609
CURRENT PILING DATE: 2005-06-24
PRIOR APPLICATION NUMBER: 10/412,000
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US-11-096-568A-20853
US-11-096-568A-34393
                                                                            ALIGNMENTS
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LOCATION: (9)
... OTHER INFORMATION: Variable amino acid
US-11-166-609-24
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OTHER INFORMATION: Variable amino acid
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. Sequence 24. Application US/11166609
. Publication No. US20060015968A1
. GENERAL INFORMATION:
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Best Local Similarity 90.0
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ORGANISM: Zea mays
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LOCATION: (7)
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LOCATION: (2)..(3)
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US-11-166-609-25
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Sequence 25378, Application US/11096568A

Sequence 25378, Application US/11096568A

Publication No. US20060048240A1

GENERAL INFORMATION:

TITLE OF INVENTION:
TITLE OF INVENTION:
THERE OF INVENTION:
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THERE OF INVENTION:
TOWERNT APPLICATION NUMBER: US/11/096,568A

CURRENT FILING DATE: 2005-04-01

SEQ ID NO 25378

LENGTH: 61
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US-11-205-109-43

Sequence 43, Application US/11205109

Publication No. US20050287641A1

GENERAL INFORMATION:

APPLICANT: Farnet, Chris

APPLICANT: Saffa, Alfredo

TITLE OF INVENTION: GENE CLUSTER FOR RAMOPLANIN BIOSYNTHESIS

FILE REPERBRUE: 3002-208

CURRENT APPLICATION NUMBER: US/09/976,059

FRIOR PELING DATE: 2001-015

PRIOR FILING DATE: 2001-015

PRIOR FILING DATE: 2001-0-15

PRIOR FILING DATE: 2001-0-15

NUMBER OF SEQ ID NOS: 46

SOFTWARE: Patentin version 3.0

SEQ ID NO 43

LENGTH: 52

TENGTH: 52
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LOCATION: (1)._(61)
OTHER INFORMATION: Ceres Seq. ID no. 12589527
## PRIOR FILING DATE: 2003-04-11
| PRIOR PLING DATE: 2000-04-11
| PRIOR PELING DATE: 2000-09-26
| NUMBER OF SEQ ID NOS: 34
| SOFTWARE: Patentin Ver. 3.3
| SEQ ID NO 25
| LENGTH: 10
| TYPE: RRT
| TYPE: RRT
| CRGANISM: Zea mays
                                                                                                                                                                                                                                                  h 100.0%;
Similarity 40.0%; 1
4; Conservative 6;
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ORGANISM: Zea mays subsp. mays
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Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 2300
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Publication No. US20060041949A1
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                     SOFTWARE: PatentIn version 3.3
SEQ ID NO 542
LENGTH: 73
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SEQ ID NO 546
LENGTH: 73
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APPLICANT: FONTANA Maria Rita
                                                                                              ORGANISM: Nicotiana tabacum
US-11-116-881A-542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-11-116-881A-546
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NUMBER OF SEQ ID NOS: 2300
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6 FGSGRRSCPG 15
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FGSGRRSCPG 15
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Best Local Similarity
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Best Local Similarity
Matches 4; Conserv
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Publication No. US20060041949A1
GENERAL INFORMATION:
APPLICANT: Xu, Dongwei
APPLICANT: Nielsen, Mark T.
TITLE OF INVENTION: Nicotiana Nucleic Acid Molecules and Uses Thereof
FILE REFERENCE: 07678/141014
CURRENT APPLICATION NUMBER: US/11/116,881A
CURRENT FILING DATE: 2005-04-27
PRIOR APPLICATION UNBER: 60,665,451
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                                         DB 7; Length 61;
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                                                                              Indels
                                                                                                                                                                                                                                       Sequence 10778, Application US/11087099; Publication No. US20060041961A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Genes and Uses for Plant Improvement; FILE REFERENCE: 38-21(53450) B FP; CURRENT APPLICATION NUMBER: US/11/087,099; CURRENT PILING DATE: 2005-03-22; SEQ ID NOS: 12464; SEQ ID NOS: 12464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IOCATION: (1). (71)
COTHER INFORMATION: unsure at all Xaa locations US-11-087-099-10778
                                                        Pred. No. 87;
6; Mismatches
                                       Score 33;
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APPLICATION NUMBER: 60/665,097
FILING DATE: 2005-03-24
APPLICATION NUMBER: 60/646,764
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APPLICATION NUMBER: 60/607,357
FILING DATE: 2004-09-03
APPLICATION NUMBER: 60/566,235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 2004-09-03
APPLICATION NUMBER: 10/943,507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 2004-09-17
APPLICATION NUMBER: 60/503,989
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APPLICATION NUMBER: 60/485,368
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APPLICATION NUMBER: 10/934,944
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APPLICATION NUMBER: 60/418,933
                                         100.0%;
                                                            40.08;
                                   Query Match
Best Local Similarity 40.0
Matches 4; Conservative
                                                                                                               1 PXXGXXXCXG 10
                                                                                                                                     3 FGGGLRFCVG 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Glycine max
 US-11-096-568A-25378
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APPLICANT: Xu, Dongmei
APPLICANT: Xu, Dongmei
APPLICANT: Xu, Dongmei
APPLICANT: Nielsen, Mark T.
TITLE OF INVENTION NICOCCIAna Nucleic Acid Molecules and Uses Thereof
FILE REFERENCE: 07678/141014
CURRENT PILING DATE: 2005-04-27
PRIOR PILING DATE: 2005-03-24
PRIOR PILING DATE: 2005-03-24
PRIOR PLILING DATE: 2005-03-24
PRIOR PILING DATE: 2005-01-25
PRIOR PILING DATE: 2005-01-25
PRIOR PILING DATE: 2006-04-29
PRIOR PILING DATE: 2004-09-03
PRIOR PILING DATE: 2003-09-18
PRIOR PILING DATE: 2003-09-18
PRIOR PILING DATE: 2003-09-08
PRIOR PILING DATE: 2003-09-09
PRIOR PILING DATE: 2003-
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100.0%; Score 33; DB 7; Length 73; 40.0%; Pred..No. 1e+02; tive .6; Mismatches 0; Indels
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Sequence 25377, Application US/11096568A

Sequence 25377, Application US/11096568A

Publication No. US20060048240A1

GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides ITILE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A

CURRENT FILING DATE: 2005-04-01
SEQ ID NO 25377

LENGTH: 99
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APPLICANT: Xu, Dongmei

APPLICANT: Xielsen, Mark T.

TITLE OF INVENTION: Nicociana Nucleic Acid Molecules and Uses Thereof

FILE OF INVENTION: Nicociana Nucleic Acid Molecules and Uses Thereof

TILE OF INVENTION: Nicociana Nucleic Acid Molecules and Uses Thereof

CURRENT APPLICATION NUMBER: US/11/116,881A

CURRENT APPLICATION NUMBER: 60/665,451

PRIOR FILING DATE: 2005-03-24

PRIOR FILING DATE: 2005-03-24

PRIOR FILING DATE: 2005-03-24

PRIOR FILING DATE: 2005-01-25

PRIOR PILING DATE: 2004-09-03

PRIOR FILING DATE: 2004-09-03

PRIOR PILING DATE: 2004-09-03

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PRIOR FILING DATE: 2004-09-03

PRIOR PILING DATE: 2004-09-03

PRIOR FILING DATE: 2003-09-08

PRIOR PILING DATE: 2003-09-08

PRIOR PILING DATE: 2003-07-08

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Pred. No. 1.2e+02;
6; Mismatches 0; Indels
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; LOCATION: (1)...(99)
; OTHER INFRAMITION: Ceres Seq. ID no. 12589526
US-11-096-5688-25377
                                                                                                     Sequence 548, Application US/11116881A Publication No. US20060041949A1 GENERAL INFORMATION:
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40.0%; F
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ORGANISM: Zea mays subsp. mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Nicotiana tabacum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 40.v.
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19 FGSGRRSCPG 28
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Pred. No. 1e+02;
6; Mismatches 0; Indels
APPLICANT: PIZZA Mariagrazia
PEPLICANT: MASIGNANI Vega
APPLICANT: MOMACI Eliaabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
SEQ ID NO 8472
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Publication No. US20060003323A1
GENERAL INFORMATION:
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; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8472
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40.0%; P
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Best Local Similarity 40.0
Matches 4; Conservative
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Best Local Similarity 40.0
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51 FPQGSGRCLG 60
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53 FLFGLQTCRG 62
                                                                                                                                                            FILE REFERENCE:
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ORGANISM:
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GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides I TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILLING DATE: 2005-04-01
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APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
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40.0%; Pred. No. 1.4e+02;
tive 6; Mismatches 0
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Pred. No. 1.4e+02;
6; Mismatches 0
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; LOCATION: (1)...(107)
; OTHER INFORMATION: Ceres Seq. ID no. 13636171
US-11-096-568A-26958
                                                                                                                             APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OP INVENTION: NOVel full length cDNA
FILER REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
NUMBER OF SEQ ID NOS: 4096
NUMBER OF SEQ ID NOS: 4096
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Publication No. US20060048240A1
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Publication No. US20050255114A1
GENERAL INFORMATION:
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ORGANISM: Zea mays subsp. mays
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40.0%; E
                                                                                    OSHIKAWA, TSUTOMU
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Best Local Similarity 40.v-
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SEQ ID NO 26958
LENGTH: 107
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Best Local Similarity 40.0
Matches 4; Conservative
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44 FSAGPRNCIG 53
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40 FRKGKEACSG 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
US-11-072-512-3124
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LENGTH: 103
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                                Gaps
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                                                                                                                                                                                                                                                                                                                                           APPLICANT: Xu, Dongmei
APPLICANT: Nielsen, Mark T.
TITLE DF INVENTION: Nicotiana Nucleic Acid Molecules and Uses Thereof
FILE REFERENCE: 07679/14101014
CURRENT APPLICATION NUMBER: US/11/116,881A
CURRENT FILING DATE: 2005-04-27
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Pred. No. 1.3e+02;
                              0; Indels
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  Pred. No. 1.3e+02; 6; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR PILING DATE: 2005-03-24
PRIOR APPLICATION NUMBER: 60/646,764
PRIOR PLIING DATE: 2005-01-25
PRIOR PLIING DATE: 2005-01-25
PRIOR PLIING DATE: 2004-09-03
PRIOR PLIING DATE: 2004-04-09
PRIOR PLIING DATE: 2004-04-09
PRIOR PLING DATE: 2004-09-03
PRIOR PLING DATE: 2004-09-03
PRIOR PLING DATE: 2004-09-03
PRIOR PLING DATE: 2004-09-03
PRIOR PLING DATE: 2004-09-13
PRIOR APPLICATION NUMBER: 10/934,507
PRIOR PLING DATE: 2003-09-18
PRIOR PLING DATE: 2003-10-16
                                                                                                                                                                                                                                                                 Sequence 2299, Application US/11116881A
Publication No. US20060041949A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/665,451
PRIOR PILING DATE: 2005-03-24
PRIOR PELING DATE: 2005-03-24
PRIOR PILING DATE: 2005-03-24
PRIOR PLICATION NUMBER: 60/646,764
PRIOR APPLICATION NUMBER: 60/646,764
PRIOR APPLICATION NUMBER: 60/607,357
PRIOR FILING DATE: 2004-09-03
PRIOR PELICATION NUMBER: 60/507,257
PRIOR PELICATION NUMBER: 60/507,257
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Publication No. US20060029945A1
GENERAL INFORMATION:
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APPLICANT: SUGIXAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: ISHII, SHIZUKO
APPLICANT: ISONO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YUKI
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40.08;
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Best Local Similarity 40.0
Matches 4; Conservative
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Best Local Similarity 40.0
Matches 4; Conservative
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NAGAI, KEIICHI
                                                                               1 PXXGXXXCXG 10
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41 FGGGLRFCVG.50
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DUBLICATION NO. US20060041949A1
| Publication No. US20060041949A1
| Publication No. US20060041949A1
| Publication No. US20060041949A1
| Publication No. US20060041949A1
| APPLICANT: Nielsen, Mark T.
| APPLICANT: Nielsen, Mark T.
| APPLICANT: Nielsen, Mark T.
| APPLICANTON: Nicotiana Nucleic Acid Molecules and Uses Thereof FILE REFERENCE: 07678/141014
| CURRENT APPLICATION NUMBER: US/11/116,881A
| CURRENT APPLICATION NUMBER: US/45/17
| PRIOR APPLICATION NUMBER: 60/665,097
| PRIOR FILING DATE: 2005-03-24
| PRIOR PILING DATE: 2005-03-25
| PRIOR APPLICATION NUMBER: 60/665,097
| PRIOR PILING DATE: 2004-09-03
| PRIOR APPLICATION NUMBER: 60/667,357
| PRIOR APPLICATION NUMBER: 60/667,357
| PRIOR APPLICATION NUMBER: 00/667,357
| PRIOR APPLICATION NUMBER: 00/607,357
| PRIOR APPLICATION NUMBER: 00/607,357
| PRIOR APPLICATION NUMBER: 00/607,369
| PRIOR PILING DATE: 2004-09-17
| PRIOR PILING DATE: 2004-09-17
| PRIOR PILING DATE: 2003-09-18
| PRIOR PILING DATE: 2003-09-18
| PRIOR FILING DATE: 2003-09-18
| PRIOR FILING DATE: 2003-09-18
| PRIOR FILING DATE: 2003-09-16
| PRIOR FILING DATE: 2003-09-16
| PRIOR FILING DATE: 2003-10-16
                 PRIOR FILING DATE: 2003-09-18
PRIOR PILING DATE: 2003-09-18
PRIOR PILING DATE: 2003-07-08
PRIOR FILING DATE: 2003-07-08
PRIOR FILING DATE: 2002-10-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2300
SOFTWARE: Patentin version 3.3
SEQ ID NO 464
LENGTH: 118
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                                                                                                                                                                                                                                                                                                                                                                                                         Score 33; DB 7; Length 118;
Pred. No. 1.5e+02;
Mismatches 0; Indels
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6; Mismatches
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; ORGANISM: Nicotiana tabacum
US-11-116-881A-460
                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Nicotiana tabacum
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.
Best Local Similarity 40.0
Matches 4; Conservative
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52 FGSGRRSCPG 61
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51 FGSGRRSCPG 60
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Best Local Similarity
Matches 4; Conserv
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APPLICANT: Xu, Dongmei
APPLICANT: Nielsen, Mark T.
TITLE OF INVENTION: Nicotelana Nucleic Acid Molecules and Uses Thereof
FILE REFERENCE: 07678/141014
CURRENT APPLICATION NUMBER: US/11/116,881A
CURRENT APPLICATION NUMBER: 06/65,451
PRIOR FILING DATE: 2005-03-24
PRIOR FILING DATE: 2005-03-24
PRIOR FILING DATE: 2005-03-24
PRIOR PLICATION NUMBER: 60/665,097
PRIOR APPLICATION NUMBER: 60/667,764
PRIOR PLING DATE: 2004-09-03
PRIOR PLING DATE: 2004-09-03
PRIOR PLING DATE: 2004-09-03
PRIOR PLING DATE: 2004-09-03
PRIOR FILING DATE: 2004-09-03
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                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 33; DB 6; Length 113;
40.0%; Pred. No. 1.5e+02;
tive 6; Mismatches 0; Indels
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Sequence 6613
; FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07;
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt_SEQ_genes Version 1.0
LENGTH: 113
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Publication No. US20060041949A1
GENERAL INFORMATION:
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Best Local Similarity 40.0%;
Marches 4; Conservative
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Conservative
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; ORGANISM: Triticum aestivum
US-11-087-099-6613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108 FDGGADSCRG 117
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56 PLSGFISCVG 65
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                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1478
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Best Local Similarity
Matches 4; Conserv
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US-11-087-099-6613
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APPLICANT: FOX, TIM
APPLICANT: FOX, TIM
APPLICANT: FOX, TIM
APPLICANT: HUFFMAN, GARY
APPLICANT: HUFFMAN, GARY
APPLICANT: TRIMMELL, MARY
TITLE OF INVENTION: WIGHER BEDIATING MALE FERTILITY AND
TITLE OF INVENTION: WETHOD OF USING SAME
FILE REPRENUE: 1148CR
CURRENT APPLICATION NUMBER: US/11/166,609
CURRENT FILING DATE: 2005-06-24
FRIOR APPLICATION NUMBER: 10/412,000
FRIOR APPLICATION NUMBER: 09/670,153
FRIOR FILING DATE: 2000-09-16
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PARENTIN VET. 3.3
SEQ ID NO 15
LENGTH: 128
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APPLICANT: Xu, Dongmei
TITLE OF INVENTION: Nicotiana Nucleic Acid Molecules and Uses Thereof
TITLE OF INVENTION: Nicotiana Nucleic Acid Molecules and Uses Thereof
TITLE OF INVENTION: Nicotiana Nucleic Acid Molecules and Uses Thereof
TITLE OF TILING DATE: 2005-04-27
PRIOR APPLICATION NUMBER: 60/665,451
PRIOR PILING DATE: 2005-03-24
PRIOR PILING DATE: 2005-01-25
PRIOR PILING DATE: 2005-01-25
PRIOR PILING DATE: 2006-01-25
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                        Length 128;
Score 33; DB 7; Length Lar.
Pred. No. 1.6e+02;
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                                                                                6; Mismatches
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; Sequence 500, Application US/11116881A
; Publication No. US20060041949A1
; GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 10/934,944
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PRIOR APPLICATION NUMBER: 60/485,368
                                                                                                                                                                                                                                                                                                                  Sequence 15, Application US/11166609
Publication No. US20060015968A1
GENERAL INFORMATION:
                        Query Match
Best Local Similarity 40.0%;
Matches 4; Conservative 6
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: ALBERTSEN, MARC C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 2004-09-03
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Best Local Similarity 40.0
Matches 4; Conservative
                                                                                                                                 1 FXXGXXXCXG 10
                                                                                                                                                                |::|::|:|
68 FQAGPRICLG 77
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68 FQAGPRICLG 77
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; ORGANISM: Zea maye
US-11-166-609-15
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APPLICANT: FOX, TIM
APPLICANT: FOX, TIM
APPLICANT: HUFFWAN, GARY
APPLICANT: HUFFWAN, GARY
TITLE OF INVENTION: METHOD OF USING SAME
FILE REFERENCE: 1148CR
FILE REFERENCE: 1148CR
CURRENT APPLICATION NUMBER: 10/412,000
PRIOR PILING DATE: 2005-06-24
PRIOR PLILING DATE: 2005-04-11
PRIOR PLILING DATE: 2000-04-11
PRIOR PLILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PATENTIN VOYER: 03/670,153
SEQ ID NO 14
LENGTH: 128
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1.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 33; DB
Pred. No. 1.6e+
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: NAGALARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: Novel full length CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: JP 2001-379298
PRIOR FILING DATE: 2001-11-05
                                                 Sequence 2610, Application US/11072512
Publication No. US20060029945A1
GENERAL INFORMATION:
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Publication No. US20060015968A1
GENERAL INFORMATION:
                                                                                                                            ISOGAI, TAKAO
SUGIYAMA, TOMOYASU
OTSUKI, TETSUJI
WAKAMATSU, AI
SATO, HIROYUKI
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YAMAMOTO, JUN-ICHI
ISONO, YUUKO
HIO, YURI
OTSUKA, KAORU
NAGAI, KEIICHI
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SEKI, NAOHIKO
YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2610
LENGTH: 126
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Best Local Similarity 40.0
Best Local Similarity 40.0
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ORGANISM: Homo sapiens
US-11-072-512-2610
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; ORGANISM: Zea maye
US-11-166-609-14
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Publication No. US20060041949A1
GENERAL INFORMATION:
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APPLICANT: Xu, Dongmei
APPLICANT: Nielsen, Mark T.
TITLE OF INVENTION: Niccitiana Nucleic Acid Molecules and Uses Thereof
TITLE OF INVENTION: Niccitiana Nucleic Acid Molecules and Uses Thereof
TILL SEFERENCE: 076-03-141014
CURRENT APPLICATION NUMBER: 08/11/116,881A
CURRENT FILING DATE: 2005-03-24
PRIOR APPLICATION NUMBER: 60/665,097
PRIOR APPLICATION NUMBER: 60/665,097
PRIOR FILING DATE: 2005-01-25
PRIOR FILING DATE: 2005-01-25
PRIOR FILING DATE: 2004-09-03
PRIOR FILING DATE: 2004-09-03
PRIOR FILING DATE: 2004-09-03
PRIOR PLILING DATE: 2003-09-18
PRIOR APPLICATION NUMBER: 60/648,368
PRIOR PLILING DATE: 2003-09-18
PRIOR PRILING DATE: 2003-09-18
PRIOR PLILING DATE: 2003-09-18
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                                                                                 Remaining Prior Application data removed - See File Wrapper or FALM. NUMBER OF SEQ ID NOS: 2300 SOFTWARE: Patentin version 3.3 SEQ ID NO 500
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NUMBER OF SEQ ID NOS: 2300
SOFTWARE: PatentIn version 3.3
SEQ ID NO 516
LENGTH: 129
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Pred. No. 1.6e+02;
6; Mismatches 0; Indels
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Pred. No. 1.6e+02;
6; Mismatches 0;
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US-11-116-881A-540
; Sequence 540, Application US/11116881A
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Sequence 516, Application US/11116881A
Publication No. US220660041949A1
GENERAL INFORMATION:
     PRIOR FILING DATE: 2003-07-08
PRIOR APPLICATION NUMBER: 60/418,933
PRIOR FILING DATE: 2002-10-16
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; ORGANISM: Nicotiana tabacum
US-11-116-881A-516
                                                                                                                                                                                                                               TYPE: PRT; ORGANISM: Nicotiana tabacum
US-11-116-881A-500
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Best Local Similarity 40.0
Matches 4; Conservative
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Best Local Similarity 40.0
Matches 4; Conservative
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103 FGSGRRSCPG 112
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62 FGSGRRSCPG 71
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APPLICANT: National Marketina Marie T.

TITLE OF INVENTION: National Marketina Marie T.

TOTAL OF INVENTION: National Marie T.

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JS-11-116-881A-462
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Publication No. US20060041949A1

GENERAL INPORMATION:

APPLICANT: Xu, Dongmei

APPLICANT: Xu, Dongmei

APPLICANT: Nielsen, Mark T.

TILLE OF INVENTION: Nicotiana Nucleic Acid Molecules and Uses Thereof

FILE REFERENCE: 076781/41014

CURRENT PILING DATE: 2005-04-27

PRIOR PILING DATE: 2005-03-24

PRIOR PLING DATE: 2004-09-03

PRIOR PLING DATE: 2004-09-03
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Publication No. US20060041949A1
GENERAL INFORMATION:
APPLICANT: Xu, Dongmei
APPLICANT: Xu, Dongmei
APPLICANT: Nielsen, Mark T.
TITLE OF INVENTION: Nicotiana Nucleic Acid Molecules and Uses Thereof
FILE REFERENCE: 07-78/141014
CURRENT APPLICATION NUMBER: US/11/116,881A
CURRENT FILING DATE: 2005-04-27
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NUMBER OF SEQ ID NOS: 2300
SOFTWARE: PatentIn version 3.3
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Pred. No. 1.7e+02;
3; Mismatches 0; Indels
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PRIOR FILING DATE: 2005-03-24
PRIOR FILING DATE: 2005-03-25
PRIOR PILING DATE: 2005-03-25
PRIOR PILING DATE: 2004-09-03
PRIOR APPLICATION NUMBER: 60/66,235
PRIOR PILING DATE: 2004-09-03
PRIOR PELING DATE: 2004-09-03
PRIOR PILING DATE: 2004-09-03
PRIOR PILING DATE: 2004-09-03
PRIOR PILING DATE: 2004-09-03
PRIOR PILING DATE: 2004-09-03
PRIOR APPLICATION NUMBER: 10/943,507
PRIOR APPLICATION NUMBER: 60/503,989
PRIOR PILING DATE: 2003-09-18
PRIOR PILING DATE: 2003-09-18
PRIOR PILING DATE: 2003-07-08
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US-11-116-881A-456
                                                                                       Query Match
Best Local Similarity 40.0
Matches 4; Conservative
; ORGANISM: Streptomyces sp.
US-11-143-980-68
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Best Local Similarity 40.0
Matches 4; Conservative
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58 FDSGLDVCCG 67
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FGPGRRSCPG 77
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US-11-116-881A-520
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Sequence 462, Application US/11116881A
Publication No. US20060041949A1
| Publication No. US20060041949A1
| GENERAL INCOMATION:
| APPLICANT: Wichen, Mark T. |
| TITLE OF INVENTION: Micotiana Nucleic Acid Molecules and Uses Thereof FILE REFERENCE: 07678/1141014
| CURRENT APPLICATION NUMBER: US/11/116,881A |
| CURRENT APPLICATION NUMBER: 60/665,451 |
| PRIOR PLIING DATE: 2005-03-24 |
| PRIOR PLLING DATE: 2005-03-24 |
| PRIOR PLLING DATE: 2005-03-24 |
| PRIOR PLLING DATE: 2005-01-25 |
| PRIOR PLLING DATE: 2005-01-25 |
| PRIOR PLLING DATE: 2004-09-03 |
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SEQ ID NOS: 2300
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                                                                                                                 APPLICATION NUMBER: 60/566,235
FILING DATE: 2004-04-29
APPLICATION NUMBER: 10/934,944
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PRIOR APPLICATION NUMBER: 10/943,507
PRIOR FILING DATE: 2004-09-17
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PRIOR APPLICATION NUMBER: 60/503,989
PRIOR FILING DATE: 2003-09-18
PRIOR APPLICATION NUMBER: 60/485,368
PLICATION NUMBER: 60/646,764
                                     FILING DATE: 2005-01-25
APPLICATION NUMBER: 60/607,357
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PRIOR APPLICATION NUMBER: 60/418,933
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PRIOR FILING DATE: 2004-09-03
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PRIOR APPLICATION NUMBER: 60/418,933
PRIOR FILING DATE: 2002-10-16
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NUMBER OF SEQ ID NOS: 2300
SOFTWARE: PatentIn version 3.3
SEQ ID NO 520
LENGTH: 137
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US-11-116-881A-520
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Best Local Similarity 40.C
Matches 4; Conservative
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71 FGVGRRICPG 80
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APPLICANT: Xu, bongmei
APPLICANT: Xu, bongmei
APPLICANT: Nielsen, Mark T.
TITLE OF INVENTION: Nicociana Nucleic Acid Molecules and Uses Thereof
TILLS OF INVENTION: Nicociana Nucleic Acid Molecules and Uses Thereof
TILLS RETERENCE: 07678/141014
CURRENT APPLICATION NUMBER: US/11/116,881A
CURRENT PILING DATE: 2005-03-24
PRIOR PILING DATE: 2005-03-24
PRIOR PILING DATE: 2005-03-24
PRIOR PILING DATE: 2005-01-25
PRIOR FILING DATE: 2006-01-25
PRIOR PILING DATE: 2004-09-03
PRIOR FILING DATE: 2003-09-18
PRIOR FILING DATE: 2003-09-18
PRIOR FILING DATE: 2003-09-08
PRIOR FILING DATE: 2003-09-08
PRIOR PRIOR PILING DATE: 2003-09-08
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PRIOR FILING DATE: 2003-07-08
PRIOR APPLICATION NUMBER: 600418, 933
PRIOR FILING DATE: 2002-10-16
PRIOR FILING DATE: 2002-10-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2300
SOFTWARE: Patentin version 3.3
SEQ ID NO 448
LENGTH: 151
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Pred. No. 1.9e+02;
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Pred. No. 1.9e+02;
5; Mismatches 0; Indels
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US-11-096-568A-12468
; Sequence 12468, Application US/11096568A
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Best Local Similarity 40.0%;
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Best Local Similarity 40.0%;
Matches 4; Conservative 6
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; ORGANISM: Nicotiana tabacum
US-11-116-881A-510
                                                                                                                                                                                                                                                                                                                                ORGANISM: Nicotiana tabacum
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86 FGAGRRICPG 95
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84 FGSGRRSCPG 93
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                                                                                                                                                                                                                                                                                                  TYPE: PRT
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APPLICANT: Nielean, Mark T.
TITLE OF INVENTION: Nicotiana Nucleic Acid Molecules and Uses Thereof
TITLE OF INVENTION: Nicotiana Nucleic Acid Molecules and Uses Thereof
FILE REFERENCE: 07678/141014
CURRENT APPLICATION NUMBER: US/11/116,881A
CURRENT FILING DATE: 2005-04-27
PRIOR PELION NUMBER: 60/665,451
PRIOR PILING DATE: 2005-03-24
PRIOR PILING DATE: 2005-01-25
PRIOR PLILING DATE: 2005-01-25
PRIOR APPLICATION NUMBER: 60/667,357
PRIOR PLILING DATE: 2004-09-03
PRIOR FILING DATE: 2004-09-03
PRIOR FILING DATE: 2004-04-29
PRIOR PLILING DATE: 2004-04-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 22, Application US/11084508

Sequence 22, Application WS/11084508

Publication No. US20050260737A1

GENERAL INFORMATION:

APPLICANT: Rahman, Raja Noor Zaliha Abd.

APPLICANT: Basri, Mahiran

APPLICANT: Hun, Chin John

TITLE OF INVENTION: Novel Lipase Gene from Bacillus sphaericus 205y

FILE REFERENCE: KAN-101

CURRENT APPLICATION NUMBER: US/11/084,508

CURRENT APPLICATION NUMBER: US/11/084,508

PRIOR APPLICATION NUMBER: US/11/084,508

PRIOR PILING DATE: 2004-03-18

PRIOR FILING DATE: 2004-03-18

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PatentIn version 3.2

LENGTH: 141
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                                                                                                                                                 Query Match

100.0%; Score 33; DB 7; Length 140;
Best Local Similarity 40.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 6; Mismatches 0; Indels
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Publication No. US20060041949A1
GENERAL INFORMATION:
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APPLICATION NUMBER: 60/485,368
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              ; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-11-116-881A-462
                                                                                                                                                                                                                                                                                                      1 FXXGXXXCXG 10
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ORGANISM: Moraxella Bp.
US-11-084-508-22
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Gaps

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APPLICANT: Nieleen, Mark T.
TITLE OF INVENTION: Nicotiana Nucleic Acid Molecules and Uses Thereof
FILE REFERENCE: 07678/141014
CURRENT APPLICATION NUMBER: US/11/116,881A
CURRENT FILING DATE: 2005-04-27
PRIOR APPLICATION NUMBER: 60/665,451
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                                                                       NAME/KEY: misc_feature
i LOCATION: (1)...(158)
cother information: Ceres Seq. ID no. 12340682
US-11-096-5688-14863
                                                                                                                                                                                                                                                 6; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/607,357
PRIOR FILING DATE: 2004-09-03
PRIOR PELICATION NUMBER: 60/566,235
PRIOR FILING DATE: 2004-04-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 10/943,507
PRIOR FILING DATE: 2004-09-17
PRIOR APPLICATION NUMBER: 60/503,989
PRIOR FLING DATE: 2003-09-18
PRIOR APPLICATION NUMBER: 60/485,368
PRIOR FILING DATE: 2003-07-08
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PRIOR APPLICATION NUMBER: 60/646,764
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PRIOR FILING DATE: 2004-09-03
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US-11-116-881A-486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2005-01-2
TYPE: PRT
ORGANISM: Zea mays subsp.
                                                                                                                                                                                                                                                 4; Conservative
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APPLICANT: Nielsen, Mark
                                                                                                                                                                                                                                                                                                                              |::|:::|:|
92 FSCGRHSCVG 101
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97 FGAGRRICPG 106
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                                                                                                                                                                                                   Query Match
Best Local Similarity
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                                   APPLICANT: Alexandrov, Nickolai et al.

TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE OF INVENTION: Therby
FILE REFERENCE: 2750-15922052
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT APPLICATION NUMBER: US/11/096,568A
SURBER FILE OF DISCOURS: 34471
SEQ ID NO 12468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IS-11-096-568A-14864
Sequence 14864, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE BEFERNCE: 2750-1592F022
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 14864
LENGTH: 156
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APPLICANT: Alexandrov, Nickolai et al.
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PM22
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 33; DB 7; Length 155;
40.0%; Pred. No. 1.9e+02;
tive 6; Mismatches 0; Indels
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40.0%; Pred. No. 1.9e+02;
tive 6; Mismatches 0
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.; OTHER INFORMATION: Ceres Seq. ID no. 14301815
US.11-096-5688-12468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION: (1)...(156)
; OTHER INFORMATION: Ceres Seq. ID no. 12340683
US-11-096-568A-14864
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; Sequence 14863, Application US/11096568A
; Publication No. US20060048240A1
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US20060048240A1
                                                                                                                                                                                                                                                                                             ORGANISM: Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.
Best Local Similarity 40.0
Matches 4; Conservative
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Best Local Similarity 40.0
Matches 4; Conservative
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5 FPRGNRLCSG 14
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LOCATION: (1)...(155)
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Gaps
PRIOR APPLICATION NUMBER: 60/485,368
PRIOR FILING DATE: 2003-07-08
PRIOR APPLICATION NUMBER: 60/418,933
PRIOR FILING DATE: 2002-10-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2300
SOFTWARE: Patentin version 3.3
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100.0%; Score 33; DB 7; Length 175;
Best Local Similarity 40.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 6; Mismatches 0; Indels
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publication No. US2006000527741
GENERAL INFORMATION:
APPLICANT: Forge, Charlie
APPLICANT: Forge, Charlie
APPLICANT: Forge, Charlie
APPLICANT: Forge, Charlie
APPLICANT: Miao, Guo-Hua
FILE OF INVENTION: CDNAS Encoding Polypeptides
FILE REPRENCE: BB-1365 US NA
CURRENT FILING DATE: 2005-05-02
FRIOR PELLOATION NUMBER: US/11/120,308
CURRENT FILING DATE: 2000-07-12
PRIOR PELLOATION NUMBER: 06/14,188
PRIOR FILING DATE: 2000-07-12
PRIOR PELLOATION NUMBER: 60/14,188
PRIOR PELLOATION NUMBER: 60/14,188
PRIOR PELLOATION NUMBER: 60/14,189
PRIOR PELLOATION NUMBER: 60/14,189
PRIOR PELLING DATE: 1999-07-12
PRIOR PELLING DATE: 1999-10-15
PRIOR PELLING DATE: 1999-07-12
                                                                                                                                                                                                                                                                                                                                                                       ) ORGANISM: Nicotiana tabacum
US-11-116-881A-470
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108 FGSGRRSCPG 117
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(170)
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                                                                                                                                                                                                                                                                 SEQ ID NO 470
LENGTH: 175
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LOCATION:
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NAME/KEY:
LOCATION:
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US-11-116-881A-470

| Sequence 470, Application US/11116881A
| Publication No. US20060041949A1
| GENERAL INPORMATION:
| APPLICANT: Xu, Dongmei
| APPLICANT: Xu, Dongmei
| TITLE OF INVENTION: NICOTIANA APPLICANTON NUMBER: US/11/116,881A
| CURRENT FILING DATE: 2005-04-27
| PRIOR PAPLICATION NUMBER: 60/665,451
| PRIOR PAPLICATION NUMBER: 60/665,097
| PRIOR PELING DATE: 2005-01-25
| PRIOR PPLING DATE: 2005-01-25
| PRIOR PLING DATE: 2004-09-03
| PRIOR PLING DATE: 2004-09-03
| PRIOR PILING DATE: 2004-09-17
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   TITLE OF INVENTION: Nicotiana Nucleic Acid Molecules and Uses Thereof
FILE REFERENCE: 07678/141014
CURRENT APPLICATION NUMBER: US/11/116,881A
CURRENT PILING DATE: 2005-04-27
PRIOR PLICATION NUMBER: 60/665,451
PRIOR PLICATION NUMBER: 60/665,097
PRIOR PLIING DATE: 2005-03-24
PRIOR PLIING DATE: 2004-09-03
PRIOR PLIING DATE: 2003-07-08
PRIOR PLIING DATE: 2003-07-08
PRIOR PLIING DATE: 2002-10-16
PRIOR PLIING DATE: 2003-07-18
PR
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: LOCATTON: (27)...(27)

: OTHER INFORMATION: Xaa = Leu, Pro, His, or Arg.

US-11-116-881A-484
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ORGANISM: Nicotiana tabacum
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FGMGRRACPG 101
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h 100.0%;
Similarity 40.0%; 3
4; Conservative 6
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                                       DATE: 2005-03-2
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127 FGAGRRICPG 136
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FCCGRFGCFG 33
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Best Local Similarity
Matches 4; Conserva
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Best Local Similarity
Matches 4; Conserv
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NUMBER OF
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APPLICANT: Xu, Dongmei
APPLICANT: Xu, Dongmei
APPLICANT: Nielsen, Mark T.
IITLE OF INVENTION: Nicotiana Nucleic Acid Molecules and Uses Thereof
FILE REFERENCE: 07678/141014
CURRENT APPLICATION NUMBER: US/11/116,881A
CURRENT PILING DATE: 2005-04-27
FRICK APPLICATION NUMBER: 60/665,451
PRICK APPLICATION NUMBER: 60/665,097
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APPLICANT: Nielsen, Mark T.
TITLE OF INVENTION: Nicotiana Nucleic Acid Molecules and Uses Thereof
FILE REFERENCE: 07678/141014
CURRENT APPLICATION NUMBER: US/11/116,881A
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                                                                                       100.0%; Score 33; DB 7; Length 176; 40.0%; Pred. No. 2.1e+02;
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2.1e+02;
ches 0; Indels
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Pred. No. 2.1e+
6; Mismatches
                                                                                                           ed. No. 2.16
Mismatches
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femaling Prior Application data removed
NUMBER OF SEQ ID NOS: 2300
SOFTWARE: PatentIn version 3:3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R FILING DATE: 2005-03-24

R APELICATION NUMBER: 60/646,764

R FILING DATE: 2005-01-25

R APELICATION NUMBER: 60/607,357

R APELICATION NUMBER: 60/566,235

R APELICATION NUMBER: 60/566,235

R APELICATION NUMBER: 10/934,944

R APELICATION NUMBER: 10/934,944

R RILING DATE: 2004-09-03

R APELICATION NUMBER: 10/934,507
                                                                                                                                                                                                                                                                                 Sequence 522, Application US/11116881A Publication No. US20060041949A1 GENERAL INFORMATION:
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APPLICATION NUMBER: 60/503,989
FILING DATE: 2003-09-18
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APPLICATION NUMBER: 60/418,933
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Best Local Similarity 40.0
Matches 4; Conservative
                                                                                                                      Conservative
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                                                                                                                                                            1 PXXGXXXCXG 10
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Best Local Similarity
Matches 4; Conserv
                NAME/KEY: UNSURE
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                                   ; LOCATION: (17
US-11-120-308-106
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FEATURE:
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### RIGHE APPLICATION WINDERS (60/650, 907)
### RIGHE APPLICATION WINDERS (60/650, 907)
### RIGHE APPLICATION WINDERS (60/60/150)
### RIGHE APPLICATION WINDERS (60/60/160)
### RESULT 41
### RESULT 4
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Sequence 1843, Application US/11096568A

Sequence 1843, Application Wo. US20060048240A1

GENERAL INFORMATION:
GENERAL INFORMATION:
HAPPLICATH: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides FI TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
TITLE OF INVENTION: 1592006-1592008.
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT PILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 18243
LENGTH: 197
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US-02-955-493-12

Sequence 12, Application US/0995493

Sequence 12, Application No. US20060035293A1

Sequence 12, Application No. US20060035293A1

Sequence 12, Application No. US20060035293A1

SEMENTAL INFORMATION:

APPLICANT: Handfield, Martin

APPLICANT: Progulake-Fox, Ann

TITLE OF INVENTION: Identification of Actinobacillus actinomycetemcomitans Antigens for INVENTION: in the Diagnosis, Treatment, and Monitoring of Periodontal Disease TITLE REFERENCE: MBHB01-65

CURRENT APPLICATION NUMBER: US/09/995,493

CURRENT FILING DATE: 2001-11-28

NUMBER OF SEQ ID NOS: 234

SEQ ID NO 12
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             100.0%; Score 33; DB 7; Length 194; 50.0%; Pred. No. 2.3e+02;
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Best Local Similarity 40.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 6; Mismatches 0; Indels
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i TYPE: PRT
i ORGANISM: Actinobacillus actinomycetemcomitans
US-09-995-493-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Zea mays subsp. mays
FRATURE:
NAME/KEY: misc_feature
COCATION: (1). (197)
OTHER INFORMATION: Ceres Seq. ID no. 12363892
US-11-096-568A-18243
                                                                                 5; Mismatches
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Best Local Similarity 40.0%;
                   Query Match 100.
Best Local Similarity 50.0
Matches 5, Conservative
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125 FGAGREXCAG 134
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154 FGAGRRMCPG 163
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                                                                                                                                                                                                                                                                                                      RESULT 44
US-11-096-568A-18243
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US-11-087-099-7405
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Publication No. US20060048240A1

GENERAL INFORMATION:

APPLICANT: Albarandrow, Nickolai et al.

TITLE OF INVENTION: Therby

TITLE OF INVENTION: Therby

TITLE OF INVENTION: Therby

CURRENT PAPLICATION NUMBER: US/11/096,568A

CURRENT PILING DATE: 2005-04-01

NUMBER OF SEQ ID NOS: 34471

SEQ ID NO 23881

LENGTH: 194
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                                                                                                     APPLICANT: Nielsen, Mark T.
APPLICANT: Nielsen, Mark T.
APPLICANT: Nielsen, Mark T.
TILLE OF INTENTION: Nicotiana Nucleic Acid Molecules and Uses Thereof
FILE REFERENCE: 07678/141014
CURRENT FILING DATE: 2005-04-27
CURRENT FILING DATE: 2005-04-27
PRIOR PILING DATE: 2005-03-24
PRIOR PILING DATE: 2005-03-24
PRIOR PLICATION NUMBER: 60/665,097
PRIOR PILING DATE: 2005-03-24
PRIOR PILING DATE: 2004-09-03
PRIOR PILING DATE: 2004-09-03
PRIOR PILING DATE: 2004-09-03
PRIOR PILING DATE: 2004-04-29
PRIOR PLILING DATE: 2004-04-29
PRIOR PLILING DATE: 2004-09-03
PRIOR PLILING DATE: 2003-09-18
PRIOR PLING DATE: 2003-09-18
PRIOR 
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NAME/KEY: misc_feature

LOCATION: (131)

OTHER INFORMATION: Xaa is any aa, unknown or other
US-11-096-568A-23881
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NAME/KEX: misc_feature
NAME/KEX: misc_feature
CATION: (1)..(194)
OTHER INFORMATION: Ceres Seq. ID no. 12416120
                   Sequence 458, Application US/11116881A
Publication No. US20060041949A1
GENERAL INFORMATION:
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ORGANISM: Zea mays subsp. mays
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ORGANISM: Nicotiana tabacum
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Matches 4; Conservative
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120 FGSGRRSCPG 129
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US-11-096-568A-23881
US-11-116-881A-458
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                                                                 Length 210;
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Publication No. US20060041961A1

GENERAL INFORMATION:

APPLICANT: Abad, Mark S. et al.

TITLE OF INVENTION: Genes and Uses for Plant Improvement;

FILE REPRENCE: 38-21(53450) B.P

CURRENT APPLICATION NUMBER: US/11/087,099

CURRENT FILING DATE: 2005-03-22

NUMBER OF SEQ ID NOS: 12464

SEQ ID NO 2635

LENGTH: 213
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GENERAL INFORMATION:
TITLE OF INVENTION: Genes and Uses for Plant Improvement; FILE REFERENCE: 38-21(53450)B EP; CURRENT APPLICATION NUMBER: US/11/087,099; CURRENT AILING DATE: 2005-03-22; NUMBER OF SEQ ID NOS: 12464; SEQ ID NO 11719
    ; OTHER INFORMATION: Xaa is any aa, unknown or other
US-11-096-568A-23880
                                                               ; Score 33; DB 7;
Pred. No. 2.5e+02;
5; Mismatches 0
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Pred. No. 2.5e+02;
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6; Mismatches
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                                                               Query Match 100.0%;
Best Local Similarity 50.0%;
Matches 5; Conservative 5
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US-11-087-099-2635
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Best Local Similarity 40.0
Eachen 4; Conservative
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Best Local Similarity 40.0
Matches 4; Conservative
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US-11-087-099-11719
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153 FNGGPRICLG 162
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Publication No. US20060048240A1
GENERAL INFORMATION:
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE REFERENCE: 2750-1592PUSZ
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 23880
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40.0%; Pred. No. 2.5e+02;
tive 6; Mismatches 0; Indels
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Sequence 11148, Application US/11087099

Publication No. US20060041961A1

GENERAL INFORMATION:

APPLICANT: Abad, Mark S. et al.

TITLE OF INVENTION: Genes and Uses for Plant Improvement

FILE REFERENCE: 38-21 (53450) B EP

CURRENT FILING DATE: 2005-03-22

NORDENT FILING DATE: 2005-03-22

NORDENT FILING DATE: 2005-03-22

LENGTH: 208
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                                                            APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FITLE REPERRICE: 38-21(53450) B. EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 7405
                                                                                                                                                                                                                                                                                                                Score 33; DB 7;
Pred. No. 2.5e+02;
6; Mismatches 0
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OTHER INFORMATION: Ceres Seq. ID no. 12416119
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ORGANISM: Phanerochaete chrysosporium
Sequence 7405, Application US/11087099
Publication No. US20060041961A1
GENERAL INFORMATION:
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; ORGANISM: Populus x canescens
US-11-087-099-7405
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Matches 4; Conservative
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136 FGAGRRMCPG 145
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143 FNAGPRICLG 152
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NAME/KEY: misc feature
LOCATION: (147)..(147)
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Best Local Similarity
Matches 4; Conserva
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S-09-315-304B-487

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US-08-484-615-208
US-08-68-71-208
US-08-724-4668-7
US-08-724-4668-7
US-08-724-4668-9
US-08-724-4668-9
US-08-724-4668-10
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US-08-882-164D-6
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US-08-102-863-2
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-07-912-900-13

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US-07-912-900-13

US-08-285-309-13

US-08-285-309-14

US-08-285-309-15

US-08-213-075A-12

US-08-113-075A-14

US-08-502-046-13

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TYPE: amino acid
STRANDEDNESS: single
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GENERAL INFORMATION:

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APPLICANT:
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Patent No. 5569832
GENERAL INFORMATION:
APPLICANT: Cornish, Edwina C.
APPLICANT: Kovacic, Filiappa
APPLICANT: Tanaka, Yoshikazu
APPLICANT: Lester, Diane R.
TITLE OF INVENTION: GENETIC SEQUENCES ENCODING A 3,5'-
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: U.S.A.
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PAETENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/912,900
FILING DATE: 19920713
FILING DATE: 19250713
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1; Mismatches
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CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Didiglio, Frank S.
REGISTRATION NUMBER: 31,346
REGISTRATION NUMBER: 8633
TELECOMMUNICATION INFORMATION:
TELEPAX: (516) 742-4346
TELER: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERSIFICS:
LENGTH: 10 amino acids
TYPE: AMINO ACID
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90.0%; F
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Best Local Similarity 90.0
Matches 9; Conservative
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FXXGXRXCXG 10
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RESULT 1
US-07-912-900-1
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CONRESPONDENCE ADDRESS:

COUNTRY (1.5 A. C.)

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Pred. No. 1e+02;
5; Mismatches 0; Indels
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Pred. No. 1e+02;
6; Mismatches 0; Indels
                                                                                                                         Sequence 129, Application US/09904615
Patent No. 6566325
GENERAL INFORMATION
TITLE OF INVENTION: 49 Human Secreted Proteins
CURRENT APPLICATION NUMBER: 0S/09/04,615
CURRENT FILING DATE: 2001-07-16
PRIOR FILING DATE: 1998-08-25
PRIOR FILING DATE: 1998-08-31
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 129
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 49 Human Secreted Proteins
FILE REFERENCE: PZ032P1
CURRENT APPLICATION NUMBER: US/10/054,988
CURRENT FILING DATE: 2002-01-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 09/904,615
PRIOR FILING DATE: 2001-07-16
PRIOR PLING DATE: 2001-07-16
PRIOR PELING DATE: 2000-02-23
PRIOR PELING DATE: 2000-02-23
PRIOR PELING DATE: 1998-08-25
PRIOR PELING DATE: 1998-08-15
PRIOR PELING DATE: 1998-08-15
PRIOR PELING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 170
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 129
LENGTH: 10
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; Sequence 129, Application US/10054988
; Patent No. 6953667
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Best Local Similarity 40.0%; Pr
Matches 4; Conservative 6;
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Best Local Similarity 40.0%;
Matches 4; Conservative 6
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                                   1 FXXGXXXCXG 10
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1 FSLGRRHCLG 10
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1 FSLGRRHCLG 10
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; ORGANISM: Homo sapiens
US-10-054-988-129
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Sequence 21, Application US/08948564
Patent No. 6121512
GENERAL INFORMATION:
APPLICANT: Siminszky, Balazs
APPLICANT: Siminszky, Balazs
APPLICANT: Corbin, Frederick T.
TITLE OF INVENTION: No. 6121512el Cytochrome P-450 Constructs and
TITLE OF INVENTION: Methods of Producing Herbicide-Resistant Transgenic Plants
NUMBER OF SEQUENCES:
ADDRESSES: Virginia C. Bennett
STREET: PO Box 37428
CITY: Raleigh
STATE: No. 6121512th Carolina
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/948,564
                                                                                                                                                                                                                                                                                                                                  ; Score 33; DB 1;
Pred. No. 1e+02;
1; Mismatches
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ZIP: 27627
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Virginia C.
REGISTRATION NUMBER: 37,092
REPERENCE/DOCKET NUMBER: 5051
TELECOMMUNICATION INFORMATION:
  Query Match
Best Local Similarity 90.0%;
Matches 9; Conservative 1
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                              single
                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
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                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: sir
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Best Local Similarity
Matches 10; Conserva
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; Sequence 15, Application US/07912900
; Patent No. 5349125
; GENERAL INFORMATION:
    APPLICANT: Holton, Timothy A. APPLICANT: Cornish, Edwina C. APPLICANT: Kovacic, Filippa APPLICANT: Tanaka, Yoshikazu APPLICANT: APPLICANT: SEQUENCES ENCODING FLAVONOID TITLE OF INVENTION: PATHWAY ENZYMES AND USES THEREFOR NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 33; DB 1; Length 11;
Pred. No. 1.1e+02;
5; Mismatches 0; Indels
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COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

FOR INTORIER: 19920713

CLASSIFICATION NUMBER: 800

ATTORNEY/AGENT INFORMATION:

NAME: Digitalio, Frank S.

REGISTRACE/DOCKET NUMBER: 8633

TELEPHONE: (516) 742-436

TELEPHONE: (516) 742-436

TELEPHONE: (516) 742-436

TELEPHONE: (516) 742-436

TELERA: 230 901 SANS UR

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: LAND ACTION ACTION

LENGTH: LAND ACTION

LENGTH: LAND ACTION

LENGTH: LAND ACTION

LENGTH: LAND ACTION

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NAME: DiGiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFRENCE/DOCKET NUMBER: 8633
TELECOMMUNICATION: TELEPHONE: (516) 742-4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
40.0%; P
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Best Local Similarity 40.0
Matches 4; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: peptide
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2 FGAGKRICPG 11
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                                      Sequence 13. Application US/07912900

Sequence 13. Application US/07912900

Patent No. 5349125

GENERAL INFORMATION:

APPLICANT: Holton, Timothy A. APPLICANT: Cornish, Edwina C. APPLICANT: Tanaka Yoshikazu

APPLICANT: Lester, Diane R.

TITLE OF INVENTION: PATHWAY ENZYMES AND USES THEREFOR NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS: 29

CORRESPONDENCE ADDRESS: 29

CONTRY: U.S.A.

ZIP: 11520

CONFUTER: U.S.A.

ZIP: 11520

COMPUTER: ENAPPA Gisk

COMPUTER: Batcherin Release #1.0, Version #1.25

CHASSIFCATION NUMBER: US/07/912,900

FILING DATE: 19920713

CLASSIFCATION NUMBER: 31,346

REGISTRATION NUMBER: 31,346

RELEFRAN: (516) 742-4343

TELEFRAN: 230 901 SANS UR

SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acide

LENGTH: 11 amino acide

LENGTH: 11 amino acide
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Patent No. 5349125

GENERAL INFORMATION:
APPLICANT: Holton, Timothy A. APPLICANT: Cornish, Edwina C. APPLICANT: Tanaka, Yoshikazu
APPLICANT: Tanaka, Yoshikazu
APPLICANT: Tanaka, Yoshikazu
APPLICANT: Tanaka, Yoshikazu
APPLICANT: Lester, Diane R.
ITILE OF INVENTION: PENTINC SEQUENCES ENCODING FLAVONOID
ITILE OF INVENTION: PETHWAY ENZYMES AND USES THEREFOR NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS: 29
CORRESPONDENCE ADDRESS: 29
CORRESPONDENCE ADDRESS: 5011v, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 11;
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40.0%; Pred. No. 1.1e+02;
tive 6; Mismatches 0
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TYPE: AMINO ACID
STRANDEDNESS: single
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Best Local Similarity 40.0
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                                 US-07-912-900-13
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Gapa

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TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-285-309-14
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1.1e+02;
ches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: GENETIC SEQUENCES ENCODING A 3,5'
TITLE OF INVENTION: HYDROXYLASE AND USES
CORRESPONDENCE: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.C.

ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/285,309
FILING DATE: 03-AUG-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Didigilio, Frank S.
REGISTRATION NUMBER: 31,346
REPERENCE/DOCKET NUMBER: 8633Z
TELEFONGUNICATION INFORMATION:
TELEFONGUNICATION INFORMATION INFORMA

; Score 33; DB 1;
Pred. No. 1.1e+02;
6; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Scully, Scott, Murphy & Presser STRET: 400 Garden City Plaza CITY: Garden City STATE: New York COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 1.16
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 13, Application US/08285309
Patent No. 556832
GENERAL INFORMATION:
APPLICANT: Holton, Timothy A.
APPLICANT: Cornish, Edwina C.
APPLICANT: Kovacic, Filippa
APPLICANT: Tanaka, Yoshikazu
APPLICANT: Lester, Diane R.
                                                                                                                                                                                                            STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-07-912-900-15
                                                                                                                                                                                                                                                                                                                                                                                                                                        40.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40.04;
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO:
                                                                                                                                                11 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.
Best Local Similarity 40.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 FXXGXXXCXG 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |::|:::|:
2 FGSGRRICPG 11
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FGAGRRGCPG 11
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Best Local Similarity
Matches 4; Conserva
                                                                                                                                                                                  TYPE: AMINO ACID
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US-08-285-309-13
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APPLICANT: Holton, Timothy A.
APPLICANT: Cornish, Edwina C.
APPLICANT: Towarish, Pilippa
APPLICANT: Tanaka, Yoshikazu
APPLICANT: Lester, Dianne R.
TITLE OF INVENTION: GENETIC SEQUENCES ENCODING A 3,5'-
                                                             APPLICANT: Holton, Timothy A.
APPLICANT: Cornish, Edwina C.
APPLICANT: Kovacic, Filiappa
APPLICANT: Tanaka, Yoshikazu
APPLICANT: Lester, Diane R.
TITLE OF INVENTION: GENETIC SEQUENCES ENCODING A 3,5'-
TITLE OF INVENTION: GENETIC SEQUENCES CONTESS OCORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/285,309
FILING DATE: 03-AUG-1994
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                               B: Scully, Scott, Murphy & Presser
400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8: Scully, Scott, Murphy & Presser
400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 1.16
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 33;
                                                                                                                                                                                                                                                                                                                                                    STATE: New York
COUNTRY: U.S.A.
ZIP: 11550
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S.
REGISTRATION NUMBER: 31.346
REFERENCE/DOCKET NUMBER: 36.32
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/08285309
Application US/08285309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEFAX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40.04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.
Best Local Similarity 40.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 FXXGXXXCXG 10
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Gaps
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UGS-01-10-75A-13

Sequence 13, Application US/08313075A

Patent No. 5639870

GENERAL INFORMATION:
APPLICANT: Holton, Timothy A.
APPLICANT: Cornible, Edwina C.
APPLICANT: Cornible, Edwina C.
APPLICANT: Tanaka, Yoshikaru
TITLE OF INVENTION: PATHWAY ENZYMES AND USES THEREFOR NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS: 56
CORRESPONDENCE ADDRESS: 56
CORRESPONDENCE ADDRESS: 56
ADDRESSE: 80-11y, Scott, Murphy & Presser
GTTY: Garden city Plaza
GOUNTRY: 1BW YORK
COMPUTER: New YORK
COMPUTER: READABLE FORM:
MEDIUM TYPE: Plopy disk
COMPUTER: Patentin Release #1.0, Version #1.25
GOFTAME: 30-NOV-1994
FILING DATE: 30-NOV-1994
GTLING DATE: 27-MAR-1992
PRIOR APPLICATION NUMBER: AU PL 1538/92
FILING DATE: 27-MAR-1993
PRIOR APPLICATION NUMBER: AU PCT/AU93/00127
FILING DATE: 27-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PCT/AU93/00127
FILING DATE: 27-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PCT/AU93/00127
FILING DATE: 27-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PCT/AU93/00127
FILING DATE: 27-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PCT/AU93/00127
FILING DATE: 27-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PCT/AU93/00127
FILING DATE: 27-MAR-1993
ATTOMATE ADSIGNATION:
TELEBHONE: (516) 742-4343
TTELECOMMUNICATION NUMBER: 31,346
RESERRATION FOR SEQ ID NO: 13:
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APPLICATION NUMBER: AU PCT/AU93/00127
FILING DATE: 25-MAR-1993
ATTOREX/AGENT INFORMATION:
NAME: DiGiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCS/DOCKET NUMBER: 9433
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 40.0%;
Matches 4; Conservative 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
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2 FGAGRRGCPG 11
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Sequence 12, Application US/08313075A

Patent No. 5639870

GENERAL INFORMATION:

APPLICANT: Holton, Timothy A.

APPLICANT: Cornish, Edwina C.

APPLICANT: Cornish, Edwina C.

APPLICANT: Tanaka, Yoshikazu

TITLE OF INVENTION: BATHWAY ENZYMES AND USES THEREFOR NUMBER OF SEQUENCES: 58

CORRESPONDENCE ADDRESS:

ADDRESSE: Scully, Scott, Murphy & Presser

CITY: Garden City Plaza

CITY: Garden City Plaza

CITY: Garden City Plaza

CITY: Garden City

STATE: New York

COMPUTER: Liso

COMPUTER: Exadable Form:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/313,075A

FILING DATE: 27-MAR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: AU PL 1538/92

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: AU PL 1538/93

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:
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                                                                                                                                            COMPUTER: LISSO
MEDIUM TYPE: Floppy disk
COMPUTER: TEM PC Compatible
COMPUTER: TEM PC Compatible
COMPUTER: TEM PC Compatible
COMPUTER: TEM PC COMPATIBLE
COMPUTER: TEM PC COMPATION
CLASSITICATION NUMBER: US/08/285,309
FILING BATE: 03-AUG-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: DIGIGALO, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 31,346
RELERA: (516) 742-4343
TELEFA: (516) 742-4343
TELEFA: (516) 742-4366
TELEFA: (516) 742-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
40.0%; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-285-309-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.
Best Local Similarity 40.0
Matches 4; Conservative
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2 FGSGRRICPG 11
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                      Garden City
                                                           New York
: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-313-075A-12
                  CITY: Gar
STATE: Ne
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
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Score 33; DB 1; Length 11; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                          APPLICANT: Holton, Timothy A.
APPLICANT: Cornish, Bdwina C.
APPLICANT: Kovacic, Filippa
APPLICANT: Tanaka, Yoshikazu
APPLICANT: Taneka, Yoshikazu
APPLICANT: Diane R.
TITLE OF INVENTION: GENERAL SEQUENCES ENCODING A 3,5'
TITLE OF INVENTION: HYDROXYLASE AND USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/502,046
FILING DATE: 14-JUL-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/285,309
FILING DATE: 03-404-1994
ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8633Z
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: U.S.A.
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Mismatches
                                                                                                                                                                              Application US/08502046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 14, Application US/08502046
Patent No. 5861487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SAS UR
INFORMATION FOR SEQ 1D NO: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40.04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
                         1 FXXGXXXCXG 10
                                                  |::|:::|:
FGSGRRICPG 11
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2 FGAGRRGCPG 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 4; Conserv
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APPLICANT:
APPLICANT:
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                                                                                                                                                                            Length 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Holton, Timothy A.
APPLICANT: Cornish, Edwina C.
APPLICANT: Tanaka, Yoshikazu
TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVON
TITLE OF INVENTION: PATHWAY ENZYMES AND USES THEREFOR NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.

ZITE: New York

COUNTRY: U.S.A.

ZITE: 11530

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,075A

FILING DATE: 30-NOV-1994

PILING DATE: 27-MAR-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PL 1538/92

PILING DATE: 27-MAR-1992

PILING DATE: 07-JAN-1993

PILING DATE: 07-JAN-1993

PILING DATE: 28-MAR-1993

ATTORNEY/AGENT INFORMATION:
NAME: DIGIGALION NUMBER: AU PCT/AU93/00127

FILING DATE: 28-MAR-1993

ATTORNEY/AGENT INFORMATION:
NAME: DIGIGALION NUMBER: 31,346

REGISTRATION NUMBER: 31,346

REGISTRATION NUMBER: 31,346

REGISTRATION NUMBER: 9433
                                                                                                                                                                       Query Match 100.0%; Score 33; DB 1; Best Local Similarity 40.0%; Pred. No. 1.1e+02; Matches 4; Conservative 6; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Scully, Scott, Murphy & Presser
400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 1.1e
6; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 14, Application US/08313075A Patent No. 5639870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (516) 742-4343
TELEFAX: (516) 742-4346
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
TWOP
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Best Local Similarity 40.0
Matches 4; Conservative
SEQUENCE CHARACTERISTICS LENGTH: 11 amino acid
                                             TYPE: amino acid
STRANDEDNESS: single
                                                                                                         , MOLECULE TYPE: protein US-08-313-075A-13
                                                                                                                                                                                                                                                                 1 PXXGXXXCXG 10
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FGAGKRICPG 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: sir
                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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US-08-313-075A-14
                                                                                         TOPOLOGY:
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Gaps
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APPLICANT: BOUNG-JUN, OH
APPLICANT: BOUNG-JUN, OH
APPLICANT: MOON, KYUNG KO
APPLICANT: YOUNG SOON KIN
TITLE OF INVENTION: A CYTCCHROME P450 GENE HIGHLY EXPRESSED IN THE
TITLE OF INVENTION: INCOMPATIBLE INTERACTION
FILE REPERENCE: 10324/P64443USO
CURRENT APPLICATION NUMBER: US/09/499,302A
CURRENT FILING DATE: 2000-02-07
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTIN VET: 2.1
ENGTHARE: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: Consensus OTHER INFORMATION: heme-binding domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/502,046
FILING DATE: 14-JUL-1995
CLASSIPICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/285,309
FILING BAPLICATION NUMBER: 08/285,309
FILING DATE: 03-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S.
REGISTRATION NUMBER: 8633Z
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEERAX: (516) 742-4343
TELEERAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TUBERT IN amino acids
TUBERT IN AUGH IN AUG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (8) OTHER INFORMATION: variable or unknown amino acid NAME/KEY: MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION: (10); OTHER INFORMATION: variable or unknown amino acid US-09-499-302A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (6) -
OTHER INFORMATION: variable or unknown amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 33; DB 1;
Pred. No. 1.1e+02;
6; Mismatches 0;
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; Sequence 3, Application US/09499302A
; Patent No. 6369212
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 40.0%; F
Matches 4; Conservative 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 FXXGXXXCXG 10
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Best Local Similarity
Matches 8; Consery
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-502-046-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
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US-08-502-046-15
i Sequence 15. Application US/08502046
j Patent No. 5861487
i GENERAL INFORMATION:
APPLICANT: Holton, Timothy A.
APPLICANT: Cornish, Edwina C.
APPLICANT: Tanaka, Yoshikazu
APPLICANT: Tanaka, Yoshikazu
APPLICANT: Tanaka, Yoshikazu
APPLICANT: Lester, Diane R.
ITILE OF INVENTION: GENETIC SEQUENCES ENCODING A 3,5'-
ITILE OF INVENTION: GENETIC SEQUENCES ENCODING A 3,5'-
ITILE OF GENETIC SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City Plaza
CITY: US-A.
STATE: New York
COUNTRY: US-A.

ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IB PC compatible
COMPUTER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 11;
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                                                                                                                                                                                                                          STREET: 400 Garden CLTY
CITY: Garden CITY
STATE: New York
STATE: 11530
COUNTRY: U.S.A.
ZIP: 11530
COMPUTER LEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/502,046
FILING DATE: 14-JUL-1995
CIASSIFICATION 800
PRIOR APPLICATION 800
PRIOR APPLICATION NUMBER: 08/285,309
FILING DATE: 03-AUG-1994
ATTOMEY/AGENT INFORMATION:
NAME: Didgidlo, Frank S.
REGISTRATION NUMBER: 98/33Z
TELECOMMUNICATION NUMBER: 98/33Z
TELEPAN: (516) 742-4343
TELEPAN: (516) 742-4346
TELEPAN: (516) 742-4366
TELEPAN: SAO 901 SANS UR
INFORMATION POR SEO ID NO: 14:
SEOUENCE CHARACTERISTICS:
                        APPLICANT: Lester, Diane R.
TITLE OF INVENTION: GENETIC SEQUENCES ENCODING A 3,5'
TITLE OF INVENTION: HYDROXYLASE AND USES
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSER: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 33; DB 1;
Pred. No. 1.1e+02;
6; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 FXXGXXXCXG 10
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2 FGAGKRICPG 11
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Best Local Similarity
Matches 4; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: si
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Sequence 19, Application US/08845161A
; Patent No. 5976850
; GENERAL INFORMATION:
    APPLICANT: Lathe, Richard
    APPLICANT: Base, Kenneth A.
    APPLICANT: Stapleton, Genevieve
    TITLE OF INVENTION: HIPPOCAMPUS-ASSOCIATED PROTEINS; DNA
    TITLE OF INVENTION: SEQUENCES CODING THEREFOR AND USED THEREOF
    NUMBER OF SEQUENCES: 45
    NUMBER OF SEQUENCES: 45
    NUMBER OF SEQUENCES: 45
    STREET: 1100 No. 5976850th Glebe Rd. 8th floor
    STREET: 1100 No. 5976850th Glebe Rd. 8th floor
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                                                                                                                 CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/845,161A

PILING DATE: 21-APR-1997

CLASSIFICATION NUMBER: US/08/845,161A

PILING APPLICATION DATE: 1957

PILING APPLICATION DATE: POCT-1995

PILING DATE: 18-OCT-1995

PILING DATE: 19-OCT-1994

ATTONNEY/AGENT INPOMBER: GB 9421093.7

PILING DATE: 19-OCT-1994

ATTONNEY/AGENT INPOMBER: 32,955

REGISTRATION NUMBER: G04-408

TELEBPHONE: 7703-816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/845,161A
FILING DATE: 21-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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APPLICATION NUMBER: PCT/GB95/02465
FILING DATE: 18-OCT-1995
ZIP: 22201-4741
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          703-816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 FXXGXXXCXG 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: VA
COUNTRY: USA
ZIP: 22201-4741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 2:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-845-161A-10
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Patent No. 5976850

GENERAL INFORMATION:
APPLICANT: Lathe, Richard
APPLICANT: Stapleton, Genevieve
TITLE OF INVENTION: HIPPOCAMPUS-ASSOCIATED PROTEINS; DNA
TITLE OF INVENTION: ABQUENCES CODING THEREFOR AND USED THEREOF
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Siminszky, Balazs
APPLICANT: Dewey, Ralph E.
APPLICANT: Corbin, Frederick T.
TITLE OF INVENTION: No. 6121512e1 Cytochrome P-450 Constructs
TITLE OF INVENTION: Methods of Producing Herbicide-Resistant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 No. 5976850th Glebe Rd. 8th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30
UNRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/948,564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 33;
                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSE: Virginia C. Bennett
STREET: PO BOX 37428
CITY: Raleigh
STATE: No. 6121512th Carolina
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 27627
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICALL..

FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Virginia C.
REGISTRATION NUMBER: 37,092
REFERENCE/DOCKET NUMBER: 5051
TELECOMMUNICATION INFORMATION:
                                                                                                                                          Sequence 20, Application US/08948564 Patent No. 6121512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80.08;
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Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 919-854-1401
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
       |:|||:||||
FGXGXRXCXG 11
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4 FGXGXRXCXG 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-845-161A-10
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Gape

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Query Match 100.0%; Score 33; DB 1; Length 14 Best Local Similarity 40.0%; Pred. No. 1.4e+02; Matches 4; Conservative 6; Mismatches 0; Indels
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-845-161A-20
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1 FGAGPRSCVG 10
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                                                                                                                                                                                                                                               1 FXXGXXXCXG 10
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1 FGSGATICPG 10
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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ZIP: 22201-4741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-845-161A-21
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                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 24
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US-08-845-161A-20

US-08-845-161A-20

Sequence 20, Application US/08845161A

Patent No. 5976850

GENERAL INFORMATION:

APPLICANT: Latch Richard

APPLICANT: Stapleton, Genevieve

TITLE OF INVENTION: SEQUENCES CODING THEREFOR AND USED THEREOF

NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRES: 45

COMPUTER READABLE FORM:

WEDIUM TYPE: Ploppy disk

COMPUTER READABLE FORM:

WEDIUM TYPE: Ploppy disk

COMPUTER: 1EM FC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Ploppy disk

CLASSIFICATION NUMBER: US/08/845,161A

FILING DATE: 21-APR-1997

PRIOR APPLICATION NUMBER: US/08/845,161A

FILING DATE: 21-APR-1997

PRIOR APPLICATION NUMBER: GB 9421093.7

FILING DATE: 19-OCT-1995

PRIOR APPLICATION NUMBER: GB 9421093.7

FILING DATE: 19-OCT-1995

PRIOR APPLICATION NUMBER: GB 9421093.7

FILING DATE: 19-OCT-1995

PRIOR APPLICATION NUMBER: GB 9421093.7

PRIOR APPLICATION NUMBER: GB 9421093.7
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 19-0CT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mary J.
REGISTRATION NUMBER: 604-408
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Wilson, Mary J. REGISTRATION NUMBER: 32,955 REFERENCE/DOCKET NUMBER: 604 TELECOMMUNICATION INFORMATION: 703-816-4000
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INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 40.0°
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 t TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-845-161A-19
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1 FGLGTSKCPG 10
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STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: PACHICATION DATA:
APPLICATION NUMBER: US/08/845,161A
FILING DATE: 13-APR-1997
PRIOR APPLICATION NUMBER: PCT/GB95/02465
FILING DATE: 18-OCT-1995
PRIOR APPLICATION NUMBER: PCT/GB95/02465
FILING DATE: 19-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mary J.
REGISTRATION NUMBER: 32,955
REFERENCE/POCKET NUMBER: 32,955
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Sequence 24, Application US/08845161A
Fatent No. 5976850
GENERAL INFORMATION:
APPLICANT: Lathe, Richard
APPLICANT: Rose, Kenneth A.
TITLE OF INVENTION: HIPPOCAMPUS-ASSOCIATED PROTEINS; DNA
TITLE OF INVENTION: SEQUENCES CODING THEREFOR AND USED THEREOF
NUMBER OF SEQUENCES: 45
CORRESPONDERSES: NIXON & VANDERHYB P.C.
STREET: 1100 No. 5976850th Glebe Rd. 8th floor
CITY: Alington
SEQUENCE: VALING OF VALING O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SUSTREENT APPLICATION DATA:
APPLICATION NUMBER: US/08/845,161A
FILING DATE: 21-APR-1997
CLASSIFICATION: A35
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/02465
FILING DATE: 18-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9421093.7
                                                                                                                                                                                                              CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/845,161A

FILING DATE: 21-APR-1997

CLASSIFICATION ATA:

APPLICATION NUMBER: PCT/GB95/02465

FILING DATE: 18-OCT-1995

PRICA APPLICATION DATA:

APPLICATION NUMBER: GB 9421093.7

FILING DATE: 19-OCT-1994

ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 33; DB 1;
Pred. No. 1.4e+02;
6; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Wilson, Mary J. REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 604
TELECOMMUNICATION:
TELEPHONE: 703-816-4000
                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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ZIP: 22201-4741
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 40.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide US-08-845-161A-23
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1 FGCGARVCLG 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
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                                                                                                             APPLICANT: Lathe, Richard
APPLICANT: Lathe, Richard
APPLICANT: Stapleton, Genevieve
APPLICANT: Stapleton, Genevieve
APPLICANT: Stapleton, Genevieve
TITLE OF INVENTION: HIPPOCAMPUS-ASSOCIATED PROTEINS; DNA
TITLE OF INVENTION: SEQUENCES CODING THEREFOR AND USED THEREOF
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSE: NIXON & VANDERHYE P.C.
STREET: 1100 No. 5976850th Glebe Rd. 8th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 33; DB 1; Length 14;
40.0%; Pred. No. 1.46+02;
tive 6; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/845,161A
FILING DATE: 21-ARR-1997
CLASSIFICATION A 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/02465
FILING DATE: 18-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9421093.7
FILING DATE: 19-OCT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 22201-4741
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 22, Application US/08845161A Patent No. 5976850 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Wilson, Mary J.
REGISTRATION NUMBER: 32,955
REPERENCE/DOCKET NUMBER: 604-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acids
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Conservative
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MOLECULE TYPE: peptide
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1 FGFGMROCLG 10
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Best Local Similarity
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Gaps
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                                           100.0%; Score 33; DB 1; Length 14; 40.0%; Pred. No. 1.4e+02; tive 6; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OCMPUTEN: PXSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 Similarity 100.0%; Score 33; DB 2; I Similarity 100.0%; Pred. No. 1.4e+02; L0; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 No. 6184350th Glebe Rd.
CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/270,751
FILING DATE: 17-Apr-2000
CLASSIFICATION: cUnknown>
PRIOR APPLICATION NUMBER: ECT/GB95/02465
APPLICATION NUMBER: PCT/GB95/02465
APPLICATION NUMBER: GB 9421093.7
FILING DATE: 19-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mary J.
REGISTRATION NUMBER: 32,955
REGISTRATION NUMBER: 32,955
REGISTRATION NUMBER: 32,955
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-270-751-10
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US-09-270-711-19
; Sequence 19, Application US/09270751
; Patent No. 6184350
                                                                                                                                                                                                                                                                                                  Sequence 10, Application US/09270751; Patent No. 6184350; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 14 amino acids
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                                             Query Match 100.
Best Local Similarity 40.0
Matches 4; Conservative
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1 FGYGVRACLG 10
                                                                                                                                        1 PXXGXXXCXG 10
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Best Local Simi]
Matches 10; (
    US-08-845-161A-25
                                                                                                                                                                                                                                                                               US-09-270-751-10
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Sequence 25, Application US/08845161A

Sequence 25, Application US/08845161A

Sequence 25, Application US/08845161A

APPLICANT: Lathe, Richard

APPLICANT: Stapleton, Genevieve

TITLE OF INVENTION: HIPPOCAMPUS-ASSOCIATED PROTEINS; DNA

TITLE OF INVENTION: SEQUENCES CODING THEREFOR AND USED THEREOF

NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:

STREET: 1100 No. 5976850th Glebe Rd. 8th floor

CITY: Arlington

STREET: VAL
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ZIP: 22201-4741

COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/845,161A
FILING DATE: 21-APR-1997
CLASSIFICATION 1435
PRIOR APPLICATION NUMBER: GE 97/GB95/02465
FILING APPLICATION NUMBER: GE 9421093.7
RIUNG APPLICATION NUMBER: GE 9421093.7
RIUNG BATE: 19-OCT-1995
RIUNG APPLICATION NUMBER: GE 9421093.7
FILING BATE: 19-OCT-1995
RIUNG APPLICATION NUMBER: GE 9421093.7
                                                                                                604-408
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REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 604-4
TELECOMMUNICATION INFORMATION:
TELEPAN: 703-816-4100
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
FILING DATE: 19-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 604-4
TELECOMMUNICATION INFORMATION:
TELEFONE: 703-816-4100
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acids
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TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.
Best Local Similarity 40.0
Matches 4; Conservative
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MOLECULE TYPE: peptide
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MOLECULE TYPE: peptide
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1 FGWGVRQCLG 10
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US-08-845-161A-25
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NAME: Wilson, Mary J.
REGISTRATION NUMBER: 32,955
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Patent No. 6184350
GENERAL INFORMATION:
APPLICANT: Lathe, Richard
Rose, Kenneth A.
Stapleton, Genevieve
                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: HIPPOCAMPI
                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION TELEPHONE: 703-816-4000
                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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SEQUENCE CHARACTERISTICS
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Best Local Similarity 40.0%;
Matches 4; Conservative
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1 FGSGATICPG 10
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                                                                                                  HIPPOCAMPUS-ASSOCIATED PROTEINS; DNA
SEQUENCES CODING THEREFOR AND USED THEREOF
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Pred. No. 1.4e+02;
6; Mismatches 0; Indels
                                                                                                                                                                                                                         8th floor
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                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 17-Apr-2000
CLASSIFICATION: <a href="https://doi.org/10/10/10/">CLASSIFICATION: <a href="https://doi.org/10/">CLASSIFICATION: <a href="https://doi.org/10/">CLASSIFICATION: <a href="https://doi.org/10/">CLASSIFICATION: <a href="https://doi.org/10/">CLASSIFICATION: <a href="https://doi.org/10/">CLASSIFICATION: <a href="https://doi.org/10/">CLASSIFICATION: <a href="https://doi.org/10/">CURRION</a>
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Rose, Kenneth A.
Stapleton, Genevieve
TITLE OF INVENTION: HIPPOCAMPUS-ASSOCIATED
                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 No. 6184350th Glebe Rd.
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ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 No. 6184350th Glebe Rd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/02465
FILING DATE: 18-OCT-1995
APPLICATION NUMBER: GB 9421093.7
FILING DATE: 19-OCT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 604-408 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Wilson, Mary J. /
                                                                                               TITLE OF INVENTION: HIPPOCAMPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20, Application US/09270751
Patent No. 6184350
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                 ZIP: 22201-4741
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy,disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: <Unknown>
                    APPLICANT: Lathe, Richard
Rose, Kenneth A
Stapleton, Gener
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 19
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ZIP: 22201-4741
COMPUTER READABLE FORM:
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Best Local Similarity 40.0
Matches 4; Conservative
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FGLGTSKCPG 10
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COUNTRY: USA
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GENERAL INFORMATION:
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ZIP: 22201-4741
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: PatentIn Release #1.0, Version #1.30
CURRITY APPLICATION DATE: US/09/270,751
FILING DATE: 17-Apr-2000
CLASSIPICATION: CURROWN>
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
CERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 33; DB 2;
40.0%; Pred. No. 1.4e+02;
tive 6; Mismatches 0
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ADDRESSER: NIXON & VANDERHYE P.C.
STREET: 1100 No. 6184350th Glebe Rd.
CITY: Arlington
                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/270,751
FILLING DATE: 17-Apr-2000
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/02465
FILLING DATE: 18-OCT-1995
APPLICATION NUMBER: GB 9421093.7
FILLING DATE: 19-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/02465
FILING DATE: 18-0CT-1995
APPLICATION NUMBER: GB 9421093.7
FILING DATE: 19-0CT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear; MOLECULE TYPE: peptide; SEQUENCE DESCRIPTION: SEQ ID NO: 20: US-09-270-751-20
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Gaps

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Length 14;
                                        Indels
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40.0%; Pred. No. 1.4e+02;
tive 6; Mismatches 0
; Score 33; DB 2;
Pred. No. 1.4e+02;
6; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 No. 6184350th Glebe Rd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 604-408
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
INFORMATION FOR SEQ ID NO: 23:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Wilson, Mary J.
REGISTRATION NUMBER: 32,955
                                                                                                                                                                                                                                                                       APPLICANT: Lathe, Richard
Rose, Kenneth A.
Stapleton, Genevieve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 24, Application US/09270751; Patent No. 6184350; GENERAL INFORMATION:
                                                                                                                                                                                                             Sequence 23, Application US/09270751; Patent No. 6184350
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lathe, Richard
                      40.08;
                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.
Best Local Similarity 40.0
Matches 4; Conservative
                                        4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Arlington STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 FXXGXXXCXG 10
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1 FGCGARVCLG 10
                                                                                1 FXXGXXXCXG 10
                                                                                                      |::|::|:|
1 FGFGMRQCLG 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
    Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 35
US-09-270-751-24
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CONDITY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: DATE: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/270,751

FILING DATE: 17-Apr-2000

CLASSIFICATION: UNMBER: PCT/GB95/02465

FILING DATE: 18-OCT-1995

APPLICATION NUMBER: GB 9421093.7

FILING DATE: 18-OCT-1994

ATTORNEY/AGENT: INFORMATION:
                                                                                                                                                                                                                                                                                             Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSES: NIXON & VANDERHYE P.C.
STREET: 1100 No. 6184350th Glebe Rd. 8th floor
CITY: Arlington
                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                               ; Score 33; DB 2;
Pred. No. 1.4e+02;
6; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Lathe, Richard
Stop, Kenneth A.
Stapleton, Genevieve
TITLE OF INVENTION: HIPPOCAMPUS-ASSOCIATED
    REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 604-408
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4100
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
ERNGTH: 14 amino acids
TYPE: amino acid
STRANDENNESS: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: WIISON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 604-408
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
INFORMATION FOR SEQ ID NO: 22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-270-751-22
                                                                                                                                                                                               TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-270-751-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 22, Application US/09270751
Patent No. 6184350
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                 100.0%; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 40.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    |::|::|:|
1 FGAGPRSCVG 10
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US-09-270-751-22
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TITLE OF INVENTION: HIPPOCAMPUS-ASSOCIATED PROTEINS; DNA SEQUENCES CODING THEREPOR AND USED THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                                                   CUMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRING DATE: 17-Apr-2000
CLASSIFICATION NUMBER: US/09/270,751
FILING DATE: 17-Apr-2000
CLASSIFICATION: CUNKNOWN>
PRIOR APPLICATION: CUNKNOWN>
PRIOR APPLICATION NUMBER: PCT/GB95/02465
FILING DATE: 18-OCT-1995
ATPLING DATE: 19-OCT-1995
ATPLING DATE: 19-OCT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 14;
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Patent No. 5204096

APPLICANT: NEURATH, ALEXANDER R.; KENT, B.H.
TITLE OF INVENTION: PRE-S GENE CODED PEPTIDE HEPATITIS B
IMMUNOGENS, VACCINES, DIAGNOSTICS, AND SYNTHETIC LIPID VESICLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 6; L.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/02465
FILING DATE: 18-OCT-1995
APPLICATION NUMBER: GB 9421093.7
FILING DATE: 19-OCT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Mismatches
                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/270,751
FILING DATE: 17-Apr-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 604-408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-270-751-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 33;
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CURRENT APPLICATION DATA:

CURLENT APPLICATION NUMBER: US/07/338,028

FILING DATE: 14-APR-1989

FILING DATE: 14-APR-1989

FRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                           NAME: Wilson, Mary J.
REGISTRATION NUMBER: 32,955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1257, Application US/09471276
Patent No. 6822072
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 703-816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Dumas Milne Edwards, J.B. APPLICANT: Duclert A.
                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 703-816-4100 INFORMATION FOR SEQ ID NO: 25: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 40.0%; Matches 4; Conservative 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 05-FEB-1985
APPLICATION NUMBER: 587,090
FILING DATE: 07-MAR-1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
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Best Local Similarity 40.0%,
                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |::|::|:|
1 FGYGVRACLG 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 FXXGXXXCXG 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LENGTH: 15
5204096-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO:22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                204096-22
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Rose, Kenneth A.
Stapleton, Genevieve
TITLE OF INVENTION: HIPPOCAMPUS-ASSOCIATED PROTEINS; DNA
SEQUENCES CODING THEREFOR AND USED THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lathe, Richard
Rose, Kenneth A.
Stapleton, Genevieve
TITLE OF INVENTION: HIPPOCARUS-ASSOCIATED PROTEINS; DNA
SEQUENCES CODING THEREFOR AND USED THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 14;
                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSE: NIXON & VANDERHYE P.C.
STREET: 1100 No. 6184350th Glebe Rd. 8th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                             COUNTRY: USA
ZIP: 22201-4741
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOOPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 33; DB 2;
Pred. No. 1.4e+02;
6; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/270,751
FILLING DATE: 17-Apr-2000
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: PCT/GB95/02465
FILLING DATE: 18-OCT-1995
APPLICATION NUMBER: GB 9421093.7
FILLING DATE: 19-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 No. 6184350th Glebe Rd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 22201-4741
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 25, Application US/09270751
Patent No. 6184350
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: <Unknown>
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mary J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                         CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 PXXGXXXCXG 10
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FGWGVRQCLG 10
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Best Local Similarity
Matches 4, Conserva
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                                                                                                                                      100.0%; Score 33; DB 1; Length 19; 40.0%; Pred. No. 1.8e+02; tive 6; Mismatches 0; Indels
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Pred. No. 1.8e+02;
6; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application PC/TUS9210885
GENERAL INFORMATION:
APPLICANT: SPAIASLANI, SIMA
TITLE OF INVENTION: EXPRESSION OF P450SOY
TITLE OF INVENTION: EXPRESSION OF P450SOY
TITLE OF INVENTION: STREPTOMYCES
NUMBER OF SEQUENCES: 11
CORRESPONDENCES: 11
CORRESPONDENCES B. I. DU PONT DE NEMOURS
ADDRESSEE: AND COMPANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch,
MEDIUM TYPE: 1.0 MB
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh System, 6.0
SOFTWARE: Microsoft Word, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10885
FILING DATE: 19921216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-484-135-27
; Sequence 27, Application US/08484135
; Patent No. 5767078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: GALLEGOS, R. THOWAS
REGISTRATION NUMBER: 32,692
REFERRENCE/DOCKET NUMBER: CR-5
TELECOMMUNICATION INFORMATION:
TELEFAN: 302-892-7342
TELEFAN: 302-892-7342
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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40.0%; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 19 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 40.0
Matches 4; Conservative
      19 amino acids
                                                                                                                                            Query Match 100.
Best Local Similarity 40.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unknown
                                           SS: unknown unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
                                                                                MOLECULE TYPE: peptide
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5 FGFGVHQCLG 14
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5 FGFGVHQCLG 14
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                        TYPE: amino acid
STRANDEDNESS: un
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCT-US92-10885-2
                                                                                                                                                                                                                                                                                                                                            PCT-US92-10885-2
                                                                                                       US-08-102-863-2
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APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6822072

PATENT NO. 6822072

CURRENT NO. 6822072

CURRENT APPLICATION NUMBER: US/09/471,276

CURRENT APPLICATION NUMBER: US/09/471,276

CURRENT APPLICATION NUMBER: 09/057,719

EARLIER APPLICATION NUMBER: 09/057,719

EARLIER FILING DATE: 1998-04-08

EARLIER PILING DATE: 1998-04-08

MUMBER OF SEQ ID NOS: 1622

SOFTWARE: Patent.pm

SEQ ID NO 1257

LENGTH: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: CONSTITUTIVE
TITLE OF INVENTION: CONSTITUTIVE
TITLE OF INVENTION: CONSTITUTIVE
TITLE OF INVENTION: STREPTOMYCES
NUMBER OF SEQUENCES: 12
CORRESPONDENCES: 12
CORRESPONDENCES: 12
ADDRESSEE: B. I. DU PONT DE NEMOURS
ADDRESSEE: AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/102,863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/807,001
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08102863
Patent No. 5466590
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: GALLEGOS, R. THOMAS
REGISTRATION NUMBER: 32,692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: CR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-7342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 302-892-7949
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 40.0
Matches 4; Conservative
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4 FFFGNSPCCG 13
                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION: -14..-1
US-09-471-276-1257
                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-102-863-2
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APPLICANT: Kashyap, Arun K.
APPLICANT: Jolliffe, Linda K.
APPLICANT: Johnson, Dana
APPLICANT: Mulcahy, Linda
TITLE OF INVENTION: Compounds and Peptides That Bind to the
TITLE OF INVENTION: Exythropoietin Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSES: Townsend and townsend and Liew
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,631
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION STAR:
APPLICATION NUMBER: US 08/155,940
FILING DATE: 13-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION UNMBER: 37,330
REGISTRATION UNMBER: 37,330
REGISTRATION UNMBER: 37,330
                  APPLICATION NUMBER: US/08/484,635
FILING DATE: 07-UNN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,940
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 16528A-43-1-1
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 543-5600
TELEFAX: (415) 543-5603
INFORMATION FOR SEQ ID NO: 208: SEQUENCE CARRACTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 208, Application US/08484631 Patent No. 5830851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 40.0%;
Matches 4; Conservative 6
                                                                                                                                                                                                                                                                                                                                                              20 amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: peptide US-08-484-635-208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |::|::|:|
8 FGPGTWDCTG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Compounds and Peptides That Bind to the TITLE OF INVENTION: Exthropoietin Receptor NUMBER OF SEQUENCES: 259
CORRESPONDENCE ADDRESS: ADDRESSE: Townsend and Townsend and Crew STREET: One Market Plaza, Steuart Street Tower CITY: San Francisco STATE: California
    GENERAL INFORMATION:

APPLICANT: Johnson, Dana L
APPLICANT: Johnson, Dana L
APPLICANT: Johnson, AGONIST PEPTIDE DIMERS
NUMBER OF INVENTION: AGONIST PEPTIDE DIMERS
NUMBER OF SEQUENCES:
ADDRESSEE: Frank S. Didiglio
STREET: 400 Garden City Plaza
CITY: Garden City
CITY: Garden City
COMPUTRY: U.S.A..
ILP: 11530
COMPUTRY: IN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CUMPUTRS: IN PC COMPATION:
PELING DATE: 07-UN-1995
CLASSIFICATION NUMBER: 31,346
REPERENCE/DOCKET NUMBER: 31,346
REPERENCE/DOCKET NUMBER: 9594
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4366
INFORWATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LINFORMATION POR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LINFORMATION POR SEQ ID NO: 27:
LENGTH: 20 amino acide
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Pred. No. 1.9e+02;
6; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wrighton, Nicholas C.
Dower, William J.
Chang, Ray S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kashyap, Arun K.
Jolliffe, Linda K.
Johnson, Dana
Mulcahy, Linda
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Best Local Similarity 40.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 FXXGXXXCXG 10
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8 FGPGTWDCTG 17
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OPERATING SYSTEM:
SOFTWARE: PatentI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fYPE: amino acid
GENERAL INFORMATION:
APPLICANT: Johnso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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Sequence 6, Application US/08724466B

Patent No. 6063606

GENERAL INFORMATION:
APPLICANT: Petkovich, P. Martin, White, Jay A.,
APPLICANT: Beckett, Barbara R., Jones, Glenville
TITLE OF INVENTION: Retinoid Metabolizing Protein
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Blake, Cassels & Graydon
STREET: Box 25, Commerce Court West
COUNTRY: Canada
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
COMPUTER: COMPAQ, IBM PC compatible
COMPUTER: WORD PERFECT
CURRENT APPLICATION NUMBER: US/08/724,466B
FILING DATE: OCCEPT 1, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/724,466B
FILING DATE: JOHN C.
REGISTRATION NUMBER: 36,424
REFERENCE/DOCKET WUMBER: 36,724
TELEPHONE: (416) B67-434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; DB 2; Length 20;
1.9e+02;
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Sequence 7, Application US/08724466B

Patent No. 6053606

GENERAL INFORMATION

APPLICANT: Petkovich, P. Martin, White, Jay A.,

APPLICANT: Beckett, Barbara R., Jones, Glenville

TITLE OF INVENTION: Retinoid Metabolizing Protein

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSE: Blake, Cassels & Graydon

STREET: Box 25, Commerce Court West

CITY: Toronto

CITY: Toronto

ZIP: M5L 1A9

CONFUTER READBLE FORM:

MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 33;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPAX: (416) 863-434
TELEFAX: (416) 863-2653
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 40.0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDENESS: Single;
TOPOLOGY: linear
US-08-724-466B-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FXXGXXXCXG 10
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2 FGGGPRLCPG 11
                   FXXGXXXCXG 10
                                         |::|:::|::|
8 FGPGTWDCTG 17
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US-08-724-466B-7
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                                                                                                                                                                                                                                                                                             RESULT 44

US-08-827-570-208

i Sequence 208, Application US/08827570

j Patent No. 598647

d GENERAL INFORMATION:
APPLICANT: Wrighton, Nicholas C.
APPLICANT: Chang, Ray S.
APPLICANT: Chang, Ray S.
APPLICANT: Chang, Ray S.
APPLICANT: Johnson, Dana
APPLICANT: Johnson, Dana
TITLE OF INVENTION: Compounds and Peptides That Bind to the
TITLE OF INVENTION: Expthropoletin Receptor
TITLE OF INVENTION: Expthropoletin Receptor
CORRESPONDENCE ADDRESS:
ADDRESSEE: Towneend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
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                                                                                                                                                                                        100.0%; Score 33; DB 1; Length 20; 40.0%; Pred. No. 1.9e+02; tive 6; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CUNTRY: USA

ZIP: 94105-1492

COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/827,570
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/484,635
FILING DATE: 07-UNN-1995
APPLICATION NUMBER: US 08/155,940
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAMME: GGATELL WACKOWSKI, EUGENIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REPERENCE/DOCKET NUMBER: 16528A-43-1-1
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 208:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.
Best Local Similarity 40.0
Matches 4; Conservative
                                                                                                                                                                                                                                  4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: peptide US-08-827-570-208
                                                                                                                          MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                             1 FXXGXXXCXG 10
                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 4; Conserve
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Gaps

0; Gaps

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Length 20;
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                                                                                                                                                                                                                                                                                     Sequence 9, Application US/08724466B
Fatent No. 6063606
GENERAL INFORMATION:
APPLICANT: Beckett, Barbara R., Jones, Glenville
ITILE OF INVENTION: Retinoid Metabolizing Protein
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSE: Blake, Cassels & Graydon
STREET: Box 25, Commerce Court West
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10, Application US/08724466B
Patent No. 6063606
GENERAL INFORMATION:
APPLICANT: Petkovich, P. Martin, White, Jay A.,
APPLICANT: Beckett, Barbara R., Jones, Glenville
TITLE OF INVENTION: Retinoid Metabolizing Protein
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 1.9e+02; 6; Mismatches 0;
                               ; Score 33; DB 2;
Pred. No. 1.9e+02;
6; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 33; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Toronto
ZIP: M5L 1A9
COUNTRY: Canada
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 MD
COMPUTER: COMPAO, IBM PC compatible
OPERATING SYSTEM: MS-DOS 5.1
SOFTWARE: WORD PERFECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,466B
FILING DATE: October 1, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/667,546
FILING DATE: June 21, 1996
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 36,424
REGISTRATION NUMBER: 36,424
TELEFRONDINICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 9:
TELEPRICE (416) 863-4344
TELEPRICE (416) 863-2653
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Blake, Cassels & Graydon
Box 25, Commerce Court West
                             Query Match
Best Local Similarity 40.0%; F
Matches 4; Conservative 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%;
Best Local Similarity 40.0%;
Matches 4; Conservative 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
                                                                                                                             1 PXXGXXXCXG 10
                                                                                                                                                        2 FSGGARNCIG 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 PXXGXXXCXG 10
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2 FGTGPRNCIG 11
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Pred. No. 1.9e+02;
6; Mismatches 0; Indels
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COMPUTER READBLE FORM:
COMPUTER READBLE FORM:
COMPUTER: Diskette, 3 1/2 inch, 1.4 Mb storage
COMPUTER: COMPAQ, IBM PC compatible
COMPUTER: WORD PERFECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,466B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Petkovich, P. Martin, White, Jay A.,
APPLICANT: Beckett, Barbara R., Jones, Glenville
TITLE OF INVENTION: Retinoid Metabolizing Protein
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Blake, Cassels & Graydon
COMPUTER: COMPAQ, IBM PC compatible OPERATING SYSTEM: MS-DOS 5.1
SOUTHAREN: WORD PERFECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,466B
PILING DATE: OCCODER 1, 1996
PILING DATE: OCCODER 1, 1996
PILING DATE: UNMBER: 08/67,546
PILING DATE: UNMBER: 08/67,546
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 36,424
REPRENCE/SDOCKET NUMBER: 50767/00004
TELEPAK: (416) 863-4344
TELEPHONE: (416) 863-4344
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 mmino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: October 1, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/667,546
FILING DATE: June 21, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunt, John C.
REGISTRATION NUMBER: 36,424
REFERENCE/DOCKET NUMBER: 57/67/00004
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Blake, Cassels & Graydon STREET: Box 25, Commerce Court West
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8, Application US/08724466B Patent No. 6063606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 40.0%;
Matches 4; Conservative 6
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INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
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TOPOLOGY: linear
US-08-724-466B-8
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TOPOLOGY: linear
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ZIP: M5L 1A9

CONDTRY: Canada
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
COMPUTER: COMPAQ, IBM PC compatible
COMPUTER: COMPAQ, IBM PC compatible
COMPUTER: COMPAQ, IBM PC compatible
SOCTWARE: WORD PERFECT

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/724,466B
FILING DATE: October 1, 1996
FILING DATE: June 21, 1996
FILING DATE: June 21, 1996
ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 36,424
REFERENCE/LOCKET NUMBER: 36,424
REFERENCE/LOCKET NUMBER: 36,434
TELEPAX: (416) 863-2653
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acide
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
US-08-724-466B-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-UB-882-164D-6
Sequence 6, Application US/0888164D
Patent No. 6306624
GENERAL INPORMATION:
APPLICANT: Petkovich, P. Martin, White, Jay A.,
APPLICANT: Beckett, Barbara R., Jones, Glenville
ITITLE OF INVENTION:
APPLICANT: Beckett, Barbara R., Jones, Glenville
ITITLE OF INVENTION:
APPLICANT: Beckett, Barbara R., Jones, Glenville
ITITLE OF INVENTION:
NUMBER OF SEQUENCES:
ADDRESSEE: Blake, Cassels & Graydon
STRET: Dataio
COUNTRY: Canada
ITY: Toronto
STATE: Ontario
COUNTRY: Canada
ITY: Toronto
STATE: Ontario
COUNTRY: Canada
ITIT: MS-1A9
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
COUNTRY: Canada
ITIT: MS-1A9
COMPUTER: COMPAQ, IBM PC compatible
OPERATING SYSTEM: MS-DOS 5.1
SOFTWARE: UNGO FERRECT
COMPUTER: Unme 25, 1997
FILING DATE: Unme 25, 1997
FILING DATE: Unme 21, 1996
ATPLICATION NUMBER: 08/657,546
FILING DATE: October 1, 1996
ATPLICATION NUMBER: 08/724,466
FILING DATE: October 1, 1996
ATPLICATION NUMBER: 36,424
REFERBNCE/DOCKET NUMBER: 50767/00010
TELECOMMUNICATION INDEMBRE: 6166 863-4344
TELERPAX: (416) 863-4263
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Best Local Similarity 40.0
Matches 4; Conservative
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US-08-882-164D-6
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information for SEQ ID NO: 6:

i SEQUENCE CHARACTERISTICS:

i LENGTH: 20 amino acids

i TYPE: amino acids

i TYPE:
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aldehyde dehydroge hypothetical prote dolichyl-diphospho general stress pro phospholipase A2 ( hypothetical prote hypothetical prote hypothetical prote hypothetical prote	hypothetical prote hypothetical prote hypothetical prote cytochrome P450 4C cytochrome P450 2C reverse transcript PilB-related prote hypothetical prote defender against c cytochrome P450 PB hypothetical 19.4K thloredoxin peroxi hypothetical prote probable fimbrial	TATA-binding trans TATA-binding trans transcription init TATA box binding p TATA-binding trans transcription init TATA-binding prore TATA-binding prote transcription fact TATA-binding prote transcription init probable TATA-bind probable TATA-bind transcription init	transcription init hypothetical prote thiamin-phosphate thiamin-phosphate probable holocytoc transcription init hypothetical prote Li protein - human conserved hypothet Li protein - human cobalamin biosyth transcription fact Li protein - human cobalamin biosyth transcription fact Li protein - human Li protein - human Li protein - human Li protein - human major surface anti
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	33 1000.	33333333333333333333333333333333333333	73 33 100.0 74 33 100.0 75 33 100.0 76 33 100.0 78 33 100.0 81 33 100.0 82 33 100.0 83 33 100.0 84 33 100.0 85 33 100.0 86 33 100.0 87 33 100.0 88 33 100.0 89 33 100.0 90 33 100.0 91 33 100.0 91 92 93 100.0 96 93 100.0 97 93 100.0
tion Ltd.  18 Seconds  gnments) on cell updates/sec	283416	cted by chance to have a of the result being printed, score distribution.	hypothetical prote cellular disintegr gp38 protein - Myc probable cytochrom hypothetical prote cytochrome P450 ho hypothetical prote probable integral hypothetical prote pypothetical prote cytochrome P450 re hypothetical prote apoptotic cell dea defender against a probable apoptotic cell dea defender against chypothetical prote defender against chypothetical prote defender against chypothetical prote probable defender defender defender defender defender defender prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote
GenCore version 5.17  Copyright (c) 1993 - 2006 Biocceleration Ltd.  in search, using sw model  rch 8, 2006, 11:20:19; Search time 38 Seconds 25:320 Million cell upv	751-235-14 CXXCXG 10 S2DX: 3 C0.0 , Gapext 0.5 seqs, 96216763 resid atisfying chosen para	Match 0% Match 100% first 100 summaries first of summaries maker of results predi or equal to the score analysis of the total summaries	29 2 A56591 47 2 148943 50 2 D72034 63 2 S09643 66 2 A83375 70 2 D82025 71 2 D82025 71 2 D82025 72 2 T17791 73 2 T17791 74 2 T17791 78 2 T17791 79 2 T17791 70 2 AE2692 103 2 AF26924 96 2 AE26924 96 2 AE26924 113 2 A54437 113 2 C54437 113 2 C54437 115 2 T19039 119 2 T17016 119 2 T19039 120 2 T39694 121 2 T39694 122 2 T38989
Copy. OM protein - protein se Run on: March	US-10 33 1 PXX BLOSU Gapop 28341 hits hits	Post-processing: Minimum Maximum Listing Database: Listing 1: pir1: 2: pir2: 3: pir3: 4: pir4: pir4: pir4: pir4: accore greater than and is derived by a wook Score Match Len No. Score Match Len	2 3 3 100 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

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## ALIGNMENTS

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A; Cross-references: UNIPROT: Q61072; UNIPARC; UP1000016CAB9; EMBL: U06145; NID: 9487138; PIDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: UNIPROT: 064229; UNIPARC: UPI000013856F; GB: AF022214; NID: 93172250; PII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Ford, M.E.; Sarkis, G.J.; Belanger, A.E.; Hendrix, R.W.; Hatfull, G.F.
J. Mol. Biol. 279, 143-164, 1998
A;Title: Genome structure of mycobacteriophage D29: Implications for phage evolution.
A;Reference number: A72800; MUID:98300335; PMID:9636706
                                                                                                                                       Riweskamp, G.; Blobel, C.P.
Proc. Natl. Acad. Sci. U.S.A. 91, 2748-2751, 1994
A;Title: A new family of cellular proteins related to snake venom disintegrins.
A;Accession: 148943
A;Accession: 148943
                                 C;Species: Mus musculus (house mouse)
C;Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 05-Oct-2004
C;Accession: 148943
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C;Date: 21-Nov-1993 #sequence_revision 17-Apr-1998 #text_change 05-Oct-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Mycobacterium phage D29
C;Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 09-Jul-2004
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C;Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein
F;8/Binding site: heme iron (Cys) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 33; DB 2; Length 47; Pred. No. 1.3e+02; 6; Mismatches 0; Indels
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cellular disintegrin-related protein 16-2 - mouse (fragment)
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A;Molecule type: DNA
A;Residues: 1.63 APTT>
A;Crose-references: UNIPARC:UP1000017A254; EMBL:X15033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 33; DB 2;
Pred. No. 1.4e+02;
6; Mismatches 0;
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40.0%; F
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Best Local Similarity 40.0
Matches 4; Conservative
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Matches 4; Conservative
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FLPGGSMCRG 44
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A;Molecule type: DNA
A;Residues: 1-50 <FOR>
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A;Molecule type: mRNA
A;Residues: 1-47 <RES>
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Cipate: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
CiAccession: A82520
Rianonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Rianonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Rylate: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Rote: for a complete list of authors see reference number A59328 below
A;Rote: for a complete list of authors see reference number A59328 below
A;Rote: for a complete list of authors see reference number A59328 below
A;Rote: for a complete list of authors see reference number A59328 below
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A;Rote: for list of authors see reference number A59328 below
A;Rote: for a complete list of authors see reference number A59328 below
A;Rote: for list of authors see reference number A59328 below
A;Rote: for Boreland
A;Authors: Rerreira, V.C.A; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Rothmatic Company
A;Authors: Rerreira, V.C.A; Ferro, J.A.; Ranga, J.S.; Franca, S.C.; Rranaes, B.C.; Adathors: Machors: Machors: M.S.; Madelra, A.M.B.N.; Madelra, A.Y.; Marcho, C.L.; Marques, M.V.; Madelra, A.M.B.N.; Madelra, A.Y.; Marcho, C.L.; Marques, M.V.; Rosa, A.J. de M.S.; de M.; de Rosa Jr., V.E.; de Santelli, R.V.; Sawasak
A;Authors: de Silve, A.C.R.; de M.; de Silve, M.R.; Verligues, V.; Rosa, A.J. de Silve, R.R.; de Silve, A.R.; Verligues, V.; Rosa, A.J. de Silve, M.R.; Verligues, V.; Rosa, A.J. de Silve, M.R.; Verligues, V.; Rosa, A.J. de Silve, M.R.; Verligues, W.R.; Silve, A.C.R.; de Silve, M.R.; Verligues, W.R.; Silve, M.R.; de Silve, M.R.; Verligues, W.R.; Silve, M.R.; Verligues, W.R.; Silve, M.R.; Verligues, W.R.; Silve, M.R.; Verligues, W.R.; Silve,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-29 <SEG>
A;Cross-treferences: UNIPROT:QO8893; UNIPARC:UPI000016BFF9; GB:S60782; NID:g385887; PIDN:
A;Notes sequence extracted from NCBI backbone (NCBIN:132107, NCBIP:132113)
C;Keywords: steroid hormone receptor
                                                                   A56591
B75 steroid receptor homolog Ms1 - tobacco hornworm (fragment)
C;Species: Manduca sexta (tobacco hornworm)
C;Species: Manduca sexta (tobacco hornworm)
C;Date: 05-0an-1996 #sequence_revision 05-Jan-1996 #text_change 09-Jul-2004
C;Accession: A56591
R;Segraves, W.A.; Woldin, C.
R;Segraves, W.A.; Woldin, C.
A;Title: The E75 gene of Manduca sexta and comparison with its Drosophila homolog.
A;Title: The E75 gene of Manduca sexta and comparison with its Drosophila homolog.
A;Steference number: A56591
A;Status: preliminary
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hypothetical protein XF2749 [imported] - Xylella fastidiosa (strain 9a5c)
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Pred. No. 1e+02;
6; Mismatches 0; Indels
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; Pred. No. 89;
6; Mismatches
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Best Local Similarity 40.0
Matches 4; Conservative
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Best Local Similarity 40.C
Matches 4; Conservative
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A,Reference number: A59328
A,Contents: annotation
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probable integral membrane protein NMA0300 (imported) - Neisseria meningitidis (strain 2;
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R.Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morell; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Mature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:084610; UNIPARC:UP100000F54FF; EMBL:U42580; NID:g4028896; PII A;Experimental source: specific host Chlorella strain NC64A C;Genetics: A;Note: a294R
                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:Q9JXB9; UNIPARC:UPI00000C487B; GB:AE002561; GB:AE002098; NID A;Experimental source: serogroup B, strain MC58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:Q9JWM3; UNIPARC:UPI00000C4944; GB:AL162752; GB:AL157959; NID A;Experimental source: serogroup A, strain Z2491
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, B.R.; Rappuoli, R.; A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
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CiDate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                    Length 71;
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Pred. No. 1.9e+02;
6; Mismatches 0;
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Pred. No. 1.9e+02;
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A;Residues: 1-74 <GRA>
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R;Graves, M.V.; Van Etten, J.L.
submitted to the EMBL Data Library, May 1999
                                                                                                                                                                                                                                                                                                                                                               100.0%;
ilarity 40.0%; |
Conservative 6
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ilarity 40.0%; I
Conservative 6
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Best Local Similarity 40.0
Matches 4; Conservative
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FKLGVYTCLG 11
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2 FKLGVYACLG
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 4; Conserv
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A Molecule type: DNA
A Residues: 1-71 <TET>
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A; Residues: 1-71 < PAR>
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A;Gene: NMB2131
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A;Gene: NMA0300
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By1003

hypothetical protein NWB2131 [imported] - Neisseria meningitidis (strain MC58 serogroup C; Species: Neisseria meningitidis
C; Species: Neisseria meningitidis
C; Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C; Accession: D91003
R; Tettelin, H; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J., Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
                                                                                                                                                                                                                                                                                                                                                                                            M.J.; Br
K.; Lim,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:Q915Y3; UNIPARC:UP10000CS0AF; GB:AE004492; GB:AE004091; NIC
A;Experimental source: strain PAO1
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathd
*Reference number: A82950; MUD:20437337; PMID:10984043
A;Accession: A83575
A;Status: preliminary
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C;Superfamily: Candida cytochrome P450 52A3; cytochrome P450 homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cytochrome P450 homolog - garden pea (fragment)
C;Species: Pisum sativum (garden pea)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: 106525
R;Frank, M.R.; Deyneka, J.M.; Schuler, M.A.
Plant Physiol. 110, 1035-1046, 11996
A;Title: Cloning of wound-induced cytochrome P450 mono-oxygenases expressed in pea.
A;Reference number: Z15734; MUID:96417083; PMID:8819874
                                                                                                                                                                                                                                                                                                                                                            C; Accession: A83575
R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, Adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
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                                                                                                                                                                                                                                                                                    hypothetical protein PA0553 [imported] - Pseudomonas aeruginosa (strain PAO1)
                                                                                                                                                                                                                                                                                                            C.Species: Pseudomonas aeruginosa
C.Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
                                                        Gaps
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     Length 63;
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Pred. No. 1.8e+02;
6; Mismatches 0; Indels
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                                                     Indels
  100.0%; Score 33; DB 2;
llarity 40.0%; Pred. No. 1.7e+02;
Conservative 6; Mismatches 0;
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A;Molecule type: mRNA
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Conservative
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Matches 4; Conservative
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1 FGYGRHACPG 10
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FCLGLAACSG 20
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FQAGPRVCLG 15
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Query Match
Best Local Similarity
Matches 4; Conserv
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A; Residues: 1-66 <STO>
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-87 <GRA>
A;Residues: 1-87 <GRA>
A;Cross-references: UNIPROT:Q84552; UNIPARC:UPI00000F617B; EMBL:U42580; NID:g4028896; PII.
A;Experimental source: specific host Chlorella strain NC64A
C;Genetics:
A;Note: a232R
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A,Residues: 1-89 < RRAA>
A,Residues: 1-89 < RRAA>
A,Residues: 1-89 < RRAA>
A,Cross-references: UNIPROT:Q40985; UNIPARC:UPI000009FA6B; EMBL:U29334; NID:g894154; PIDNICSSuperfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C,Superfamily: human cytochrome P450 CYP2D6; cytochrome p450 homology
C,Keywords: chromoprotein; electron transfer; heme; iron; monooxygenase; oxidoreductase
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C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AEZ692
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.B.; Chen, Y.; Woo, Lerge, G.; Giller, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell: Science 294, 2317-2323, 2001
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A;Experimental source: strain C58 (Dupont)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drobable cytochrome P450 - garden pea (fragment)
N;Contains: oxidoreductase (EC 1.....)
C;Species: Pisum sativum (garden pea)
C;Species: Pisum sativum (garden pea)
C;Accession: T06524
R;Frank, M.; Deyneka, J.M.; Schuler, M.A.
Piant, Physiol: 110, 1035-1046, 1996
Pilant Physiol: 110, 1035-1046, 1996
A;Fitle: Cloning of wound-induced cytochrome P450 mono-oxygenases expressed in pea.
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A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CS8
A,Reference number: AB2577; MUID:21608550; PMID:11743193
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100.0%; Score 33; DB 2; Length 96;
Best Local Similarity 40.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 6; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                            Length 87;
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Pred. No. 2.2e+02;
6; Mismatches 0;
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40.0%; P
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Best Local Similarity 40.0.
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Best Local Similarity 40.03
Matches 4; Conservative
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FRSGRRGCPG 34
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A;Molecule type: DNA
A;Residues: 1-96 <KUR>
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary
A;Status: preliminary
A;Residues: 1-78 «FIN»
A;Cross-references: UNIPARC;UPI0000178A85; EMBL:AF055909; NID:GJ264593; PIDN:AAC24568.1;
C;Genetics:
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C;Genetics:
A;Start codon: GTG
                                                                                                                                                                                                                                                                                                                                            approtric cell death regulator DAD1 homolog - maize (fragment)
N;Alternate names: apoptosis suppressor; defender against cell death 1 protein
C;Species: Zea mays (maize)
C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 31-Dec-2004
C;Accession: T01646
R;Finkelstein, D.B.; Drew, M.C.; Jordan, W.R.; Wing, R.A.; Mullet, J.E.; Morgan, P.W. submitted to the EMBL Data Library, March 1998
A;Description: Apoptotic gene discovery in maize.
A;Reference number: Z14356
A;Accession: T01646
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T17723
T17723
T17723
C19724
C5 Species: Chlorella virus PBCV-1
C5 Species: Chlorella virus PBCV-1
C5 Species: Chlorella virus PBCV-1
C7 Species: Chlorella virus PBCV-1
R5 Species: T17723
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C;Species: phage phi-C31
R;Species: phi-C31
R;Spec
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40.0%; Pred. No. 2.1e+02;
tive 6; Mismatches 0;
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                                                                                                                       16 FFKGASTCEG 25
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23 FLSGVLSCIG 32
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Best Local Similarity
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T.; Kuraoka, A.; Fukushima, K.; Shibata, Y.; Komiyama, S.; Ni
                                A;Reference number: A54437; MUID:94019310; PMID:8413235
                                                                                                                                                                 A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-113 cNAK>
A;Cross-references: UNIPROT:P61803; UNIPARC:UPI0000040DF; GB:D15057; NID:g493244; PIDN:E
A;Cross-references: UNIPROT: Fransformed Raj! cells
A;Roperimental source: transformed Raj! cells
A;Note: sequence extracted from NCBI backbone (NCBIN:137990, NCBIP:137993)
C;Superfamily: Defender against cell death DAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      apoptotic cell death regulator DADI - golden hamster
Cispecies: Mesocricetus auratus (golden hamster)
Cipate: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 31-Dec-2004
CiAccession: 654437
R:Nakashima, T.; Sakiguchi, T.; Kuraoka, A.; Fukushima, K.; Shibata, Y.; Komiyama, S.; Ni
Mol. Cell. Biol. 13, 6367-6374, 1993
A;Title: Molecular cloning of a human cDNA encoding a novel protein, DADI, whose defect of A;Reference number: A54437; MUID:94019310; FMID:8413235
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A;Residues: 1.113 <NUAK>
A;Residues: 1.113 <NUAK>
A;Cross-references: UNIPROT:P61806; UNIPARC:UPI00000040DF; GB:D15058; NID:g493235; PIDN:E
A;Experimental source: BHK21 cell line
C;Superfamily: Defender against cell death DAD
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C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 31-Dec-2004
C;Accession: 149285; S6568
C;Accession: 149285; S6568
A;Apte, S.S.; Mattei, M.G.; Seldin, M.F.; Olsen, B.R.
FBBS Lett. 363, 304-306, 1995
A;Title: The highly conserved defender against the death 1 (DAD1) gene maps to human chro
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A;Residues: 1-113 <APT>
A;Cross-references: UNIPARC:UP10000047517; GB:U22107; NID:g849126; PIDN:AAA85855.1; PID:<
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ilarity 40.0%; Pred. No. 2.7e+02;
Conservative 6; Mismatches 0
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Best Local Similarity 40.0%;
Matches 4; Conservative
                          R;Nakashima, T.; Sekiguchi, T.
Mol. Cell. Biol. 13, 6367-6374
A;Title: Molecular cloning of
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56. PLSGFISCVG 65
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56 FLSGFISCVG 65
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C; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C; Accession: B89294
R; Glass, J.I.; Lefkowitz, B.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H. submitted to GenBank, February 2000
A; Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min A; Reference number: A82870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Cross-references: UNIPROT:Q9RZ12; UNIPARC:UPI00000D3B6F; GB:AE001827; NID:g6460959; PI
A,Experimental source: strain R1
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T.; Zalewski, C.; Ma
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                                                                                                                                                                                                                         C;Species: Deinococcus radiodurans
C;Dacesolon: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: A75635
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dc, M.; Shen, M.; Yanathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalc, Science 286, 1571-1577, 1999
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C;Date: 13-Sep-1994 #sequence_revision 18-Nov-1994 #text_change 31-Dec-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                           cytochrome P450-related protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein UU225.1 [imported] - Ureaplasma urealyticum
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Pred. No. 2.7e+02;
6; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
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40.0%; Pred. No. 2.5e+02;
iive 6; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   apoptotic cell death regulator DAD1
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Best Local Similarity 40.0.
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Best Local Similarity 40.0
Local 4; Conservative
2
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18 FLIGVVLCFG 27
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63 FGKGEHACLG 72
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FXXGXXXCXG
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FVFGILGCLG
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A, Genome: plasmid
A, Note: plasmid CP1
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A;Molecule type: DNA
A;Residues: 1-112 <GLA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-103 <WHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Status: preliminary
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C,Genetics: A,Gene: DRC0001

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A; Gene: UU225.1

RESULT 18

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C,Genetics

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A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C., C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Il ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                        A,Cross-references: UNIPROT:Q39080; UNIPARC:UPI0000162F4A; GB:AE005172; NID:g10801366; PJI
C,Genetics:
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A;Experimental source: strain Granny Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cydecesion: T39694

Riwood, V.; Skelton, J.; Churcher, C.M.; Rajandream, M.A.; Barrell, B.G.

Riwood, V.; Skelton, J.; Churcher, C.M.; Rajandream, M.A.; Barrell, B.G.

Riwood, V.; Skelton, J.; Churcher, C.M.; Rajandream, M.A.; Barrell, B.G.

Riwelecule to the EMBL Data Library, July 1999

A;Reference number: Z21870

A;Residues: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-119 <WGO>

A;Cross-references: UNIPROT:Q9UUP4; UNIPARC:UPI00006A199; EMBL:AL109652; PIDN:CAB51761.

A;Experimental source: strain 972h-; cosmid c17A3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       defender against cell death 1 homolog - apple tree
C;Species: Malus domestica (apple tree)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Dec-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gape
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A;Description: An apple mRNA with high homolgy to the human DAD-1 gene.
A;Reference number: Z18653
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 33; DB 2; Length 115; 40.0%; Pred. No. 2.8e+02; ive 6; Mismatches 0; Indels
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Pred. No. 2.9e+02;
6; Mismatches 0;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-119 <DON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Map position: 1
C;Superfamily: Defender against cell death DAD
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C;Superfamily: Defender against cell death DAD
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40.0%; P
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4; Conservative
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63 FLSGVLSCIG 72
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FLSGVLSCIG 68
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Best Local Similarity
Matches 4; Conserv
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A;Molecule type: DNA
A;Residues: 1-115 <STO>
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                                                                                                                                                                                                                                                                                A; Accession: F86446
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Cispectes: Oriza oriza sativa (rice)
Cispectes: Oriza sativa (
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change 31-Dec-2004
C;Date: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change 31-Dec-2004
C;Accession: S71269
R;Cooke, M.R.
submitted to the EMBL Data Library, February 1996
A;Reference number: S71269
A;Reference number: S71269
A;Residues: 11-15 < COO>
A;Residues: 11-15 < COO>
A;Residues: 11-15 < COO>
A;Cross-references: UNIPROT: 039080; UNIPARC: UPI0000128DE1; EMBL: X95585; NID: 91184192; PIC;Superfamily: Defender against cell death DAD
C;Superfamily: Defender against cell death DAD
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C'Species: Arabidopsis thaliana (mouse-ear cress)
C'Species: Oz-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2004
C'SACCESSION: F86446
R'Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Ancher 408, 816-820, 2000
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               Score 33; DB 2; Length 113;
Pred. No. 2.7e+02;
6; Mismatches 0; Indels
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Best Local Similarity 40.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 6; Mismatches 0;
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40.0%; Pred. No. 2.8e+02;
tive 6; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                  probable apoptotic cell death regulator DAD1 - rice
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                          100.08;
                                                                 40.08;
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                   Query Match
Best Local Similarity 40.0
Matches 4; Conservative
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FLSGVLSCIG 68
                                                                                                                                                                         1 FXXGXXXCXG 10
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58 FLSGVLSCIG 67
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56 FLSGFISCVG
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A; Introns: 23/1; 28/1; 59/2; 66/1

1 PXXGXXXCXG 10 |::|::|:| 44 FVPGCLLCGG 53

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C;Accession: T05467
R;Bevan, M.; Wedler, H.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Schuelle: submitted to the Protein Sequence Database, February 1998
A;Accession: T05467
A;Accession: T05467
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C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997.#text_change 09-Jul-2004
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997.#text_change 09-Jul-2004
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997.#text_change 09-Jul-2004
R;Algar, B.M.; Cheung, B.; Hayes, J.; Holmes, R.S.; Beacham, I.R.
Adv. Exp. Med. Biol. 328, 153-157, 1993
AyTitle: Bovine corneal aldehyde dehydrogenases: evidence for multiple gene products (ALI A;Reference number: 146935; MUID:93263009; PMID:8493893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:P52476; UNIPARC:UP10000129261; GB:S61045; NID:g300403; PIDN:?
C;Superfamily: NAD-dependent aldehyde dehydrogenase; aldehyde dehydrogenase homology
                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:Q9UUH1; UNIPARC:UP1000069E76; EMBL:AL109832; PIDN:CAB52733.
A;Experimental source: strain 972h-; cosmid c630
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                                                                                                                           ď
                                                                   ypothetical protein T805.60 - Arabidopsis thaliana
;Species: Arabidopsis thaliana (mouse-ear cress)
;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
al protein SPAC630.11 - fission yeast (Schizosaccharomyces pombe)
Schizosaccharomyces pombe
                                                             Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:049708; UNIPARC:UP100000A83C8; EMBL:AL021890
A;Experimental source: cultivar Columbia; BAC clone T805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Map position: 1
A;Introns: 6/2; 12/3; 37/1; 59/2; 78/1
C;Superfamily: Saccharomyces probable membrane protein YJR044c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
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Pred. No. 3e+02;
6; Mismatches 0
                                                                                                                                                                                     A;Accession: T38989
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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A;Introns: 40/2; 92/3
A;Note: T805.60
C;Superfamily: hypothetical protein YCL033c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 40.0%;
4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 40.0%;
Matches 4; Conservative
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67 FTFGATICTG 76
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51 FDDGIYSCAG 60
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                       ;Residues: 1-122 <MCD>
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A; Residues: 1-126 < ALG>
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                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: Wycobacterium leprae
C;Species: Wycobacterium leprae
C;Species: Wycobacterium leprae
C;Accession: H87152
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hcem, M.A.; Eutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq. A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Accession: H87152
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A;Cross-references: UNIPROT:O14238; UNIPARC:UPI0000130EE7; EMBL:Z98981; PIDN:CAB11729.1;
A;Experimental source: strain 972h-; cosmid c6F6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:Q9CBH8; UNIPARC:UP100000C6E17; GB:AL450380; NID:g13093604;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable oligosaccharyl transferase epsilon subunitdefender against cell death homolog C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Dec-2004
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R;Gentles, S.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V. submitted to the EMBL Data Library, September 1997
A;Reference number: Z21797
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100.0%; Score 33; DB 2; Length 119;
Best Local Similarity 40.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 6; Mismatches 0; Indels
                                                                Length 119;
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                                                          Query Match

100.0%; Score 33; DB 2;
Best Local Similarity 40.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 6; Mismatches 0
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40.0%; Pred. No. 2.9e+02;
iive 6; Mismatches 0
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A;Molecule type: DNA
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1 PXXGXXXCXG 10

8 g

Matches

A; Residues: 1-119 <STO> A; Status: preliminary A; Molecule type: DNA

A;Gene: ML1949

C; Genetica

|::|::|:| 2 FWVGVRGCGG 11

RESULT 27

A;Introns: 101/2 C;Superfamily: Defender against cell death DAD

A;Gene: SPDB:SPAC6F6.05

A; Map position: 1

A; Accession: T39039

4; Conservative

Query Match Best Local Similarity Matches 4; Conserva

1 PXXGXXXCXG 10 |::|:::|:| FLSGFISCVG 67

RESULT 28 T38989

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A;Cross-references: UNIPARC:UPI0000168417; EMBL:275010; NID:g1420282; PIDN:CAA99300.1; Pl
A;Experimental source: strain S288C.
C;Genetics:
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A;Cross-references: UNIPROT:P80242; UNIPARC:UPI0000602B3; GB:Z99110; GB:AL009126; NID:g:
A;Experimental source: strain 168
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C; Species: O7-Apr-1994 #sequence revision 19-May-1994 #text_change 05-Oct-2004
C; Accession: S22388; S36686; S36686; S36686; B. Strukelj, B.; Ritonja, A.; Gubensek, F. Bur. J. Biochem. 204, 1057-1062, 1992
Bur. J. Biochem. 204, 1057-1062, 1992
A; Title: Amino acid and cDNA sequences of a neutral phospholipase A(2) from the long-nosmathaces and an acid and cDNA sequences of periods A; Accession: S22388; MUID:92201190; PMID:1551386
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C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                           C,Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein $5.5-71/Domain: transmembrane #status preddicted <TM1>
F;55-71/Domain: transmembrane #status preddicted <TM2>
F;79-95/Domain: transmembrane #status preddicted <TM2>
F;113-129/Domain: transmembrane #status preddicted <TM3>
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                                                                                                                                                                                                               A;Cross-references: SGD:S0005629
A;Map position: 15R
C;Superfamily: Defender against cell death DAD
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C;Superfamily: hypothetical protein yklA
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Best Local Similarity 40.v.
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FLAGFIICVG 89
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                                                                                                                                                                     A; Gene: SGD:OST2; OST2
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Best Local
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A; Residues: 1-133 cabn.
A; Residues: 1-133 cabn.
A; Collins, D., Collins, P.G.; Kelleher, D.J.; Gilmore, R.
B; Silberstein, S.; Collins, P.G.; Kelleher, D.J.; Gilmore, R.
B; Silberstein, S.; Collins, P.G.; Kelleher, D.J.; Gilmore, R.
B; Silberstein, S.; Collins, P.G.; MulD:96017708; PMID:7593165
A; Residues: Scalas
A; Residues: S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypochetical protein R04ES.1 - Caenorhabditis elegans
C;Species: Caenorhabditis
C;Species: Caenorhabditis
C;Accession: T28875
R;Miller, N.
Bubmitted to the EMBL Data Library, December 1995
A;Description: The sequence of C. elegans cosmid R04ES.
A;Reference number: Z20535
A;Re
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                                                                             Length 126;
                                                                                                                                                                                0; Indels
                                                                        ; Score 33; DB 2;
Pred. No. 3e+02;
6; Mismatches 0;
                                                                             100.0%;
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Best Local Similarity 40...
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Matches 4; Conservative
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77 FECGPWTCFG 86
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24 FSMGQCCCPG 33
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A; Residues: 1-133 <VOS>
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C; Date: 16-Peb-2001 #sequence_revision 16-Peb-2001 #text_change 09-Jul-2004
C; Accession: G85060
R; Anonymous, The Buropean Union Arabidopsis Genome Sequencing Consortium, The Cold Spring Nature 402, 769-777, 1999
A; Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A; Reference number: A85001; MUID: 20083488; PMID: 10617198
                                                                                                                                                                                                                                                                                                                                                   Cross-references: UNIPROT: Q9ZS91; UNIPARC: UPI00000A7821; GB: NC_001268; NID: 97267241; P1
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C;Pate: 16-Peb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: B85060
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprinc Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
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R;Bevan, M.; Wedler, H.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Schuelle:
Bubmitted to the Protein Sequence Database, Pebruary 1998
A;Reference number: Z15417
A;Accession: T05465
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C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 139;
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Pred. No. 3.3e+02;
6; Mismatches 0;
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Pred. No. 3.3e+02;
6; Mismatches 0;
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A;Map position: 4
C;Superfamily: hypothetical protein YCL033c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C, Superfamily: hypothetical protein YCL033c
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Best Local Similarity 40.0%;
Matches 4; Conservative
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Matches 4; Conservative
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44 FEEGIFDCVG 53
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44 FEEGIFSCIG 53
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A;Molecule type: DNA
A;Residues: 1-139 <STO>
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A; Introns: 37/2; 89/3
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A; Residues: 1-11, S', 133-137 «GUB»
A; Residues: 1-11, S', 133-137 «GUB»
A; Cross-references: UNIPARC: UPI0000175886; EMBL: X56878; NID: g64450; PIDN: CAA40200.1; PID
C; Superfamily: Phospholipase A2
C; Keywords: calcium; calcium binding; carboxylic ester hydrolase; venom
F; 1-16/Domain: signal sequence #status predicted «SIG»
F; 17-137/Product: ammodytin I2 #status predicted «MAT»
F; 17-137/Product: ammodytin I2 #status predicted «MAT»
F; 13, 45, 47, 64/Binding site: calcium (Tyr, Gly, Gly, Asp) #status predicted
F; 63, 105/Active site: His, Asp #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein SMa0537 [imported] - Sinorhizobium meliloti (strain 1021) magaplasm C;Species: Sinorhizobium meliloti
C;Species: Sinorhizobium meliloti
C;Species: Sinorhizobium meliloti
C;Species: Old #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Accession: A59237
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowe A; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C. Proc. Natl. Acad. Sci. U.S.A. 98, 9839, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot
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A;Molecule type: DNA
A;Rosidues: 1-137 <KUR>
A;Cross-references: UNIPROT:0930B7; UNIPARC:UPI00000CB042; GB:AE006469; PIDN:AAK64939.1;
A;Experimental source: strain 1021, megaplasmid pSymA
B;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, P.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner S.; Wells, D.H.; Wong, K.; Yeh, K. A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A$6039; MUID:21368234; PMID:11474104
                                                              Cross-references: UNIPROT:P34180; UNIPARC:UP10000131159; EMBL:X56878; NID:95702035; P1
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G85060
hypothetical protein A74g04830 [imported] - Arabidopsis thaliana
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3.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 33; DB 2;
40.0%; Pred. No. 3.2e+02;
iive 6; Mismatches 0;
                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, January 1991
A;Reference number: $36685
A;Accession: $36685
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                                                                                                                      A;Status: preliminary
A;Modecule type: protein
A;Rediques: 17-137 (xRz>
A;Cross-references: UNIPARC:UP10000175885
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Best Local Similarity 40.0
Matches 4; Conservative
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Best Local Similarity 40.0
Matches 4; Conservative
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84 FENGDIVCGG 93
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Molecule type: mRNA;Residues: 1-137 <KRI>
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A;Gene: SMa0537
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A;Cross references: UNIPROT:0924W4; UNIPARC:UPI0000DAF25; EMBL:AL035654; PIDN:CAB38591.1
A;Experimental source: strain A3(2)
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R;Bevan, M.; Wedler, H.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Schueller
Bubmitted to the Protein Sequence Database, February 1998
A;Reference number: Z15417
A;Accession: T05466
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C;Species: Mastotermes darwiniensis (termite)
C;Species: Mastotermes darwiniensis (termite)
C;Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004
C;Accession: PC4428
B;Falckh, P.H.J.; Balcombe, W.; Haritos, V.S.; Ahokas, J.T.
Biochem. Biophys. Res. Commun. 241, 579-583, 1997
A;Title: Isolation and identification of a cytochrome P450 sequence in an Australian text.
A;Reference number: PC4428; MUID:98086394; PMID:9425314
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R;Saunders, D.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, March 1999
A;Reference number: Z21604
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C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
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X;Residues: 1-13 <BEV.
A;Cross-references: UNIPROT:O49707; UNIPARC:UPI00009E636; EMBL:AL021890
A;Experimental source: cultivar Columbia; BAC clone T805
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C;Superfamily: human cytochrome P450 CYP4BI; cytochrome P450 homology
C;Keywords: chromoprotein; heme; iron; metalloprotein
P;140/Binding site: heme iron (Cys) (axial ligand) #status predicted
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Best Local Similarity 40.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 6; Mismatches 0; Indels
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                                                                                                                        A;Accession: T36312
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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FNGGDSGCVG 84
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Best Local Similarity
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A; Residues: 1-144 < FAL>
                                                                                                                                                                                                                                  A; Residues: 1-142 <SAU>
                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: SCOEDB:SCE8.13c
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A;Introns: 39/2; 91/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein A74904840 [imported] - Arabidopsis thaliana C, Species: Arabidopsis thaliana (mouse-ear cress) C, Species: Arabidopsis thaliana (mouse-ear cress) C, Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004 C, Accession: H85060 R; Anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin Nature 402, 769-777, 1999 A; Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana. A; Reference number: A85001; MUD:20083488; PMID:10617198
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: L5-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T26567
R;White, S.
B;White, S.
B
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C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T36312
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                                                                                   100.0%; Score 33; DB 2; Length 141; 40.0%; Pred. No. 3.3e+02; Live 6; Mismatches 0; Indels
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               C; Superfamily: hypothetical protein YCL033c
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Best Local Similarity 40.0
Matches 4; Conservative
                                                                                          Query Match
Best Local Similarity 40.0
Matches 4; Conservative
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FHYGVFACEG 132
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48 FEEGTYSCAG 57
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48 FEEGIYCCVG 57
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A/Molecule type: DNA
A/Residues: 1-141 <STO>
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T36312
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Chardson, D.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P. I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-493, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; WUID:20406833; PMID:10952301
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A;Title: Isolation of a candidate gene for Norrie disease by positional cloning.
A;Reference number: S30388; MUID:93265103; PMID:1303235
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Cipate: 0.2 Feb-2001 #sequence_revision 02-Feb-2001 #text_change 31-Dec-2004
CiAccession: F84769
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Nexin, X.; Kaul, S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
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A;Cross-references: UNIPARC:UP10000178A87; GB:AE002093; NID:g3608136; PIDN:AAC36169.1; GR
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A;Residues: 1-157 <BER>
A;Cross-references: UNIPARC:UP1000011DF5F; EMBL:X65724; NID:g29946; PIDN:CAA46640.1; PID
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C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
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C.Date: 07-Oct-1994 #sequence_revision 17-Nov-1995 #text_change 08-Oct-1999
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Pred. No. 3.6e+02;
6; Mismatches 0;
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Pred. No. 3:4e+02;
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6; Mismatches
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Best Local Similarity 40.0%; | Matches 4; Conservative 6
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nes 4; Conservative
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114 FPLGSQCCLG 123
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58 FEPGLYQCAG 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-148 <HEI>
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                                                                                                                                                                                                                                                                                                                                                                                                        A, Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: S30389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: VC1236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Matches
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Biochem. Biophys. Res. Commun. 146, 224-231, 1987
A;Title: Characterization of rabbit cytochrome P450IIC4 cDNA and induction by phenobarbi
A;Reference number: S16715; MUID:87270743; PMID:3453118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-145 <ZHA1>
A;Crose-references: UNIPROT:Q29507; UNIPARC:UPI0000086985; EMBL:M17026; NID:g164932; PIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology C;Keywords: chromoprotein; electron transfer; endoplasmic reticulum; heme; iron; metalld F;90/Binding site: heme iron (Cys) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            reverse transcriptase-like protein - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Date: 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: 836442
R;Szemraj, J.; Plucienniczak, G.; Jaworski, J.; Plucienniczak, A.
R;Szemraj, A
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GB2223
PilB-related protein VC1236 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
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                                                                                                                                                                                                                                                                                                                                                      cytochrome P450 2C4 - rabbit (fragment)
N;Alternate names: cytochrome P450PBc4
N;Contains: oxidoreductase (EC 1.....)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus euniculus (domestic rabbit)
C;Date: 23-Apr-1993 #sequence_revision 23-Apr-1993 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Length 145;
    0; Indels
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A;Cross-references: UNIPARC:UPI0000174CD4; EMBL:M17026
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40.0%; Pred. No. 3.4e+02;
tive 6; Mismatches 0;
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A;Reference number: $20227
A;Accession: $20227
Mismatches
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Best Local Similarity 40.0
Matches 4; Conservative
4; Conservative
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133 FSAGPRNCIG 142
                                                                               1 FXXGXXXCXG 10
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83 FSAGKRMCVG 92
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FEIGKGVCOG 34
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Best Local Similarity
Matches 4; Conserv
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A;Molecule type: DNA
A;Residues: 1-147 <SZE>
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A, Gene: CYP2C4

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RESULT 50
155299
cytochrome P450 PB-1 - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Accession: 155299
R;Kimura, H.; Sogawa, K.; Sakai, Y.; Fujii-Kuriyama, Y.
J; Biol. Chem. 264, 2318-2342, 1989
A;Title: Alternative applicing mechanism in a cytochrome P-450 (P-450PB-1) gene generates A;Reference number: 155299; MUID:89123309; PMID:2914909
A;Status: prellminary; translated from GB/EMBL/DDBJ
A;Accession: 155299
A;Status: prellminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-169 <RES>
A;Cross-references: UNIPROT:Q64614; UNIPARC:UP10000DE6356; GB:M24239; NID:g341144; PIDN:C;Genetics:
A;Introns: 62/3; 110/1
C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C;Keywords: chromoprotein; heme; iron; mecalloprotein; transmembrane protein
F;114/Binding site: heme iron (Cys) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cyclothrome P450 monooxygenase (EC 1.-.-.) BF6-2 - fruit fly (Drosophila melanogaster) (Species: Drosophila melanogaster C;Species: Drosophila melanogaster C;Species: Drosophila melanogaster C;Species: Drosophila melanogaster C;Cpate: 28-May-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004 C;Date: 28-May-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004 C;Date: 28-May-1996 C;Date: 28-May-1996 C;Date: 28-May-1996 C;Date: 28-May-1996 C;Date: 28-May-1997 C;Date:
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                                                                                                                                                                              Query Match 100.0%; Score 33; DB 2; Length 160; Best Local Similarity 40.0%; Pred. No. 3.7e+02; Matches 4; Conservative 6; Mismatches 0; Indels
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A;Gene: At2g35520
A;Map position: 2
C;Superfamily: Defender against cell death DAD
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107 FSAGKRMCAG 116
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104 FLSGVLSCIG 113
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95 FGDGPRNCIG 104
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human papil chimpanzee human papil homo sapien pinus taeda pinus taeda povine papi musca domes

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Q53ya3 Q8miz0 Q58d69 Q5xm75

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Q76BJ9_HPBV0
Q7THR3_HPBV0
Q80GT7_HPBV0
Q8AZ65_HPBV0
Q8B4D4_HPBV0
                                                                      Q4SGY2_TETNG
Q67NC4_SYMTH
Q40986_PEA
Q9JWM3_NEIMA
Q9JXB9_NEIMB
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Q8J2R1_9PAPI
Q9Q2R1_9PAPI
Q9G2R0_HUWAN
Q5ID67_PINTA
Q5ID67_PINTA
Q5ID67_PINTA
Q5ISP98_MUSDO
Q4FCQ9_BUSGR
Q94R16_PLAFE
Q9YH76_PLAFE
Q5YH76_PLAFE
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Q4TDK7_TETNG
Q7Y2F7_9CAUD
DAD1_MAIZE
Q570F4_ARATH
Q63NDQ_BURPS
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Q9DKQ0_HPBV0
                                                                                                                       HUMAN
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42 ONCMY

Q5XNS9 PY
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homo sapien
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mus spretus
bacteriopha
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oryctolagus
mus musculu
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mus musculu
mus musculu
homo sapien
gossypium b
gossypium b
gossypium r
bacillus li
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musca domes
hepatitis b
globodera r
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crassostrea
alstroemeri
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scophthalmu
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homo sapien
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                                                     Search time 229 Seconds (without alignments) 30.809 Million cell updates/sec
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- 2006 Biocceleration Ltd
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OPPSXI XYLFA
O19047 XXLFA
O10047 XALFA
O51804 XATH
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O5185 HWAN
O54812 COSBA
O64812 COSBA
O64812 FOSE
O65253 BPICLD
VG38 BPIM2
O738 BPIM2
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09TX62 HELVI
06V0Y8 MUSSP
COATI BPIF1
09P9XI XYLFA
019047 RABIT
06LBR9 MOUSE
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8GXD1 ARATH
58F97 MUSDO
81160 HPBV0
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Q9TXO4 CHITE
Q16868 HUMAN
Q75MK4 HUMAN
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Maximum Match 100%
Listing first 100 summaries
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Q58F97_7
Q81160_F
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        GenCore (c) 1993
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1: uniprot_sprot:*
2: uniprot_trembl:*
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length: 2000000000
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33
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No.
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**ALIGNMENTS** 

SOURCE SERVING SOURCE S

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Mus spřetus (Western wild mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 33; DB 2; Length 30; 40.0%; Pred. No. 3.6e+02; Live 6; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00086; CYTOCHROME P450; UNKNOWN 1.
Heme; Iron; Metal-binding; Monooxygenase; Oxidoreductase.
NON TER
                                                                                                                                                                                                                                                                            30 AA; 3290 MW; D3A0937E3E70515E CRC64;
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                               Cytochrome P450 4a10 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Coat protein C, polypeptide I. Name=VII; Synonyms=7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00465; EP450IV.
PRINTS; PR00385; P450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Conservative
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FSGGARNCIG 20
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                                                                                                                                                                    Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00067; p450;
                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10868;
                                                                            Name=Cyp4a10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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COAT1_BPIF1
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MEDLINE-94178422; PubMed=8131898;
MEDLINE-94178422; PubMed=8131898;
Hodgson E., Rose R.M.;
Hodgson E., Rose R.L., Goh D.K., Rock G.C., Roe R.M.;
"Insect cytcohrome P-450: metabolism and resistance to insecticides.";
Biochem. Soc. Trans. 21:1060-1065(1993).
GO; GO:0060118; P:electron transport; IEA.
InterPro; IPR001128; Cytcohrome P450.
SEQUENCE 21 AA; 2422 WW; DF21177CB719B5F2 CRC64;
                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=96083592; PubMed=7493025; Watkins H., Conner D., Thierfelder L., Jarcho J.A., MacRae C., Watkins H., Conner D., Thierfelder L., Jarcho J.A., MacRae C., McKenna W.J., Maron B.J., Seidman J.G., Seidman C.E.; Mutations in the cardiac myosin binding protein-C gene on chromosome 11 cause familial hypertrophic cardiomyopathy."; Nat. Genet. 11:434-437(1995).

EMBL; S80805; AAB35661.1; -; mRNA.

NON TER 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Cytochrome P-450 (Fragment).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea; Noctuidae; Heliothinae; Heliothis.
Noctuidae; Heliothinae; Heliothis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 33; DB 2; Length 18; Best Local Similarity 40.0%; Pred: No. 2.38+02; Matches 4; Conservative 6; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 33; DB 2; Length 21;
40.0%; Pred. No. 2.6e+02;
ive 6; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE 18 AA; 1891 MW; 3EC842CE85A19C97 CRC64;
                                                                                                       Q13665;
01-NOV-1996 (TEMBLrel. 01, Created)
01-NOV-1996 (TEMBLrel. 01, Last sequence update)
01-NOV-1998 (TEMBLrel. 08, Last annotation update)
Cardiac myosin binding protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30 AA
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QCVOY8;
05-JUL-2004 (TrEMBLrel. 27, Created)
                                                                                  PRT;
                                                                       Q1365_HUMAN PRELIMINARY;
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Matches 4; Conservative
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2 FDGGIYVCGG 11
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FCLGPRNCIG 17
                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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Q6V0Y8_MUSSP
                                                          HUMAN
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Gaps

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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                              NUCLEOTIDE SEQUENCE [GENOMIC DNA].
Hill D.F., Hughes G., McNaughton J.C., Stockwell P.A., Petersen G.B.;
"DNA sequence of the filamentous coliphage If1.";
submitted (OCT-1993) to the EMBL/GenBank/DBJ databases
-!- SUBUNIT: Coat protein C is composed of two subunits, polypeptide I
(gene VII) and polypeptide II (gene IX) (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E0365E0A002B50AA CRC64;
Bacteriophage If1.
Viruses; ssDNA viruses; Inoviridae; Inovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, U02303, AAC62152.1, -; Genomic_DNA.
Capsid protein; Structural protein.
SEQUENCE 32 AA; 3394 MW; E0365E0A002B
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Matches 4; Conserv
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8

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euceleoscomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Lagomorpha; Leporidae;
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                                                                                                                                                     100.0%;
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Q9S918;
                                                                                                                                                                                                                                                                                                           QELBR9 MOUSE PRELIMINARY;
                                                                                                                                                                                  4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
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FQHGNHCCSG
                                                                    NUCLEOTIDE SEQUENCE
                                                                                                                                                     Query Match
Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                      NCBI_TaxID=9986;
                              Oryctolagus.
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Q9S9I8_ARATH
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Q6LBR9_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
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                                                                                                                                                                                                                                                                                  STRAIN=9a5C;
MEDLINE=20365717; PubMed=10910347; DOI=10.1038/35018003;
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PIR; A82520; A82250.
Complete proteome; Hypothetical protein.
SEQUENCE 35 AA; 3787 WW; D84CD0D69718029E CRC64;
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Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                                35 AA
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6; Mismatches
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                                                                                                                            Created)
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019047;
01-047;
01-JAN-1998 (TEMBLEE]. 05, C:
01-JAN-1998 (TEMBLEE]. 05, Li
01-JAN-1998 (TEMBLEE]. 05, Li
0RF36.
                                                                                                                      01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2000 (TrEMBLrel. 15, 01-JUN-2003 (TrEMBLrel. 24,
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                                                                                                                                                                                                                            Kanthomonadaceae; Xylella.
                                                                                                                                                                                 OrderedLocusNames=Xf2749;
Xylella fastidiosa.
                                                                                             QPPSX1 XYLPA PRELIMINARY;
Q9P9X1;
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PXXGXXXCXG 10
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FDAGAAICVG 14
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14 FNAGLVICFG 23
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                                                                                                                                                                  Hypothetical protein
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                                                                                                                                                                                                                                          MCBI_TaxID=2371;
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Matches
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019047 RA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
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PubMed=2584927; DOI=10.1084/jem.170.6.1837;
Brorson K.A., Hunt S.W. III, Hunkapiller T., Sun Y.H., Cheroutre H., Nickerson D.A., Hood L., "Comparison of exon 5 sequences from 35 class I genes of the BALB/c
                                                                                                                                                                                                                 Gapa
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
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Stengelin S., Becker W., Maier M., Rosenberger J., Kramer W., Submitted (OCT-1997) to the RBIL/Genbank/DBJ databases. EMBL, AJ002005; CAA05134.1; -; Genomic DNA. SEQUENCE 36 AA, 3844 WW; SBE72DD29C85E956 CRC64;
                                                                                                                                               Length 36;
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                                                                                                                                               ; Score 33; DB 2; Length 36
Pred. No. 4.3e+02;
6; Mismatches 0; Indels
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Modification methylase (Eragment)
methyltransferase) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brorson K.;
Submitted (AUG-1989) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38 AA; 4176 MW; 25428879345A1085 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          254200...
Score 33; DB 2; Lens
No. 4.5e+02;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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6; Mismatches
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NON_TER 1
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Z2 GOSBA
Q84NZ2 GOSBA PRELIMINARY;
Q84NZ2;
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7 FQHGNHSCSG 16
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18 FAVGVNICLG 27
                     Mus musculus (Mouse)
                                                                                         NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                NUCLEOTIDE SEQUENCE
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nes 4; Conserv
                                                                                                       STRAIN=Domesticus;
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                                                                   NCBI_TaxID=10090;
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NON TER
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Q84NZ2 GOS
ID Q84NZ
AC Q84NZ
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GO; GO:0005615; C:extracellular space; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                    Gaps
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                                         MEDLINE=93201384; PubMed=8389441;
Pinnegan E.J., Dennis E.S.;
"Isolation and identification by sequence homology of a putative
cytosine methyltransferase from Arabidopsis thaliana.";
Nucleic Acids Res. 21:2383-2388(1993).
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eurosids II; Brassicales; Brassicaceae; Arabidopsis
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                                                                                                                                                                                                                                             100.0%; Score 33; DB 2; Length 40; 40.0%; Pred. No. 4.7e+02; Live 6; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Phosphodiesterase I/nucleotide pyrophosphatase (Fragment)
Name=Enpp2; Synonyms=Npps2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44 AA; 4840 MW; 905EB935D7F1BF1F CRC64;
                                                                                                                                                                                                                        40 AA; 4448 MW; 33A7296755138EA7 CRC64;
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Last sequence update)
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                                                                                                               GO, GO:0005634; C:nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0006306; P:DNA methylation; IEA.
InterPro; IPR001525; CS_DNA meth.
Pfam; PF00445; DNA methylame; 1.
PROSITE; PS00094; \(\overline{CS_MINASE_1}; 1.\)
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QGLBR7 MOUSE
ID QGLBR7,
AC QGLBR7,
DT OS-JUL-2004 (TrEMBLrel. 27,
DT 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                       Q9R1DS MOUSE PRELIMINARY;
Q9R1DS;
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Best Local Similarity 40.0°
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Matches 4; Conservative
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2 FINGGPPCOG 11
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18 FAIGVNLCLG 27
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                                   NUCLEOTIDE SEQUENCE.
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            NCBI_TaxID=3702;
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Q9R1D5_MO
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Phosphodiesterase I alpha (Fragment).
Homo sapiens (Human)
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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"Molecular cloning and chromosomal assignment of the human brain-type phosphodiesterase 1/nucleotide.";
Genomics 30:380-384 (1995).
EMBL; D45914; BAA08342.1; -; Genomic_DNA.
                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                 PubMed=2584927; DOI=10.1084/jem.170.6.1837;
Brotseon K.A., Hunt S.W. III, Hunkapiller T., Sun Y.H., Cheroutre H.,
Nickerson D.A., Hood L.;
"Comparison of exon 5 sequences from 35 class I genes of the BALB/c
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MEDLINE=96163899; PubMed=8586446;
Kawagoe H., Soma O., Goji J., Nishimura N., Narita M., Inazawa J.,
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Submitted (AUG-1989) to the EMBL/GenBank/DDBJ databases.
EMBL; X16200; CAE82022.1; -; Genomic_DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44 AA; 5026 MW; 13ADBEC0561DA4D6 CRC64;
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Q1 class I MHC gene (exon 5) (Fragment).
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Q14555;
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Matches 4; Conservative
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100.0%;
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Q84NZ4 9ROSI
ID Q84NZ4 9ROSI PRELIMINARY;
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Q84NZ5 9ROSI
ID Q84NZ5 9ROSI PRELIMINARY;
                                                      Query Match
Best Local Similarity 40.0
Matches 4; Conservative
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     147
                                                                                                               1 FXXGXXXCXG 10
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13 FGAGRRICAG 22
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FGAGRRICAG
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MEDLINE-22569057; PubMed=12679546; DOI=10.1093/molbev/msg065;
Senchina D.S., Alvarez I., Cronn R.C., Liu B., Rong J., Noyes R.D.,
Paterson A.H., Wing R.A., Wilkins T.A., Wendel J.F.;
"Rate variation among nuclear genes and the age of polyploidy in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Senchina D.S., Alvarez I., Cronn R.C., Liu B., Rong J., Noyes R.D., Paterson A.H., Wing R.A., Wilkins T.A., Wendel J.F., "Rate variation among nuclear genes and the age of polyploidy in
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MR-2004 (TrEMBLrel. 26, Last annotation update)
01-MR-2004 (TrEMBLrel. 26, Last annotation update)
Putative flavonoid 3-hydroxylase (Fragment).
Gossypium barbadense (Sea-island cotton) (Egyptian cotton).
Eukaryota, Virigiplantae; Streptophyra, Embryophyta; Tracheophyta;
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MRR-2004 (TrEMBLrel. 26, Last amontation update)
01-MRR-2004 (TrEMBLrel. 26, Last amontation update)
Putative flavonoid 3-hydroxylase (Fragment)
Gossypium barbadense (Sea-island cotton) (Egyptian cotton)
Eukarycar, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22569057; PubMed=12679546; DOI=10.1093/molbev/msg065;
                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 33; DB 2; Length 47; Pred. No. 5.5e+02; 6; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00463; EP4501.
PROSITE; PS00086; CYTOCHROME_P450; 1.
Heme; Iron; Metal-binding; Monooxygenase; Oxidoreductase.
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                                                                                                                                                                                                                       MOI. Biol. Evol. 20:633-643(2003).
-!- SIMILARITY: Belongs to the cytochrome P450 family.
EMBL. AF52594, AAP05784.1; -; Genomic_DNA.
GO; GO:0066872; F:metal ion binding; IEA.
GO; GO:0004497; F:monoxygenase activity; IEA.
GO; GO:0066118; P:electron transport; IEA.
InterPro: IPR001128; Cytochrome_P450.
InterPro: IPR001218; Cytochrome_P450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gestypium.";
Mol. Biol. Evol. 20:633-643(2003).
-- SIMILARITY: Belongs to the cytochrome P450 family.
-- SIMILARITY: Belongs to the cytochrome P450 family.
GO; GO:0046872; F:metal ion binding; IEA.
GO; GO:006487; F:metal ion binding; IEA.
GO; GO:006118; F:electron transport; IEA.
InterPro; IPR001128; Cytochrome_P450.
                                                                                                                                                                                                                                                                                                                                                                                                                       47 AA; 5120 MW; 8A53B1DCB6D67951 CRC64;
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PRINTS; PR00463; EP4501.
PROSITE; PS00086; CYTOCHROME_P450; 1.
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Q84NZ3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 40.0
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13 FGAGRRICAG 22
                                                                                                                                                                                                                                                                                                                                   Pfam; PF00067; p450;
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                                                                                                            NCBI_TaxID=3634;
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                                                                                                                                                                                                             Gossypium.";
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22569057; PubMed=12679546; DOI=10.1093/molbev/msg065; Senchina D.S., Alvarez I., Cronn R.C., Liu.B., Rong J., Noyes R.D., Paterson A.H., Wing R.A., Wilkins T.A., Wendel J.P., "In Reference of among nuclear genes and the age of polyploidy in
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II, Malvales, Malvaceae, Malvoideae, Gossypium.
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II, Malvales, Malvaceae, Malvoideae, Gossypium.
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                                                                Score 33; DB 2; Length 47;
Pred. No. 5.5e+02;
6; Mismatches 0; Indels
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Heme; Iron; Metal-binding; Monooxygenase; Oxidoreductase.
NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLI Biol. Evol. 20:633-643(2003).
-1- SIMILARITY: Belongs to the cytochrome P450 family.
EMBL. AF525942; AAP05782.1; -; Genomic_DNA.
GO; GO:0064872; F:metal ion binding; IEA.
GO; GO:0004497; F:monooxygenase activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR001128; Cytochrome_P450.
InterPro; IPR001219; Cytochrome_P450.
47 AA; 5106 MW; 8A53B1DCB6D7C951 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2004 (TrENBLrel. 24, Last sequence update)
Putative flavonoid 3'-hydroxylase (Fragment).
Buberner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-UDN-2003 (TrEMBLrel. 24, Created)
01-UDN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Putative flavonoid 3'-hydroxylase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      47 AA
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01-JUN-2003 (TrEMBLrel. 24, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                          MEDLINE-98300335; PubMed-9636706; DOI=10.1006/jmb1.1997.1610; Ford M.E., Sarkis G.J., Belanger A.E., Hendrix R.W., Hatfull G.F., "Genome structure of mycobacteriophage D29: implications for phage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Cytochrome P450 related protein (Fragment).
Cytostrean gigas (Pacific oyster).
Eukaryota, Metazca; Mollusca; Bivalvia; Pteriomorphia; Ostreoida; Ostreoidea; Crassostrea.
                                                                                                Mycobacteriophage D29.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Crassostrea gigas: a new approach to better understanding primary cell culture."; Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.—; SIMILARITY: Belongs to the cytochrome P450 family. BMBL; AF075692; AA013473.1; -; mRNA. GO; GO:004697; F:metal ion binding; IEA. GO; GO:000497; F:monoxygenase activity; IEA. GO; GO:000118; P:electron transport; IEA. InterPro; IPR002401; EP4501.
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                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
  Last sequence update)
Last annotation update)
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PIR; D72804; D72804.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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40.0%;
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15-DEC-1998 (Rel. 37, La
10-MAY-2005 (Rel. 47, La
Gene 38 protein (Gp38).
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PRINTS; PR00463; EP450I
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FALGLTACDG 22
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Best Local Similarity
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                                                                                                                                                                       NCBI_TaxID=28369;
                                                                                                                                                      L5-like viruses.
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                                                                                                                                                                                                                                                                                                                              evolution."
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                           Senchina D.S., Alvarez I., Cronn R.C., Liu B., Rong J., Noyes R.D., Paterson A.H., Wing R.A., Wilkins T.A., Wendel J.F., "Rate variation among nuclear genes and the age of polyploidy in
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     MEDLINE=22569057; PubMed=12679546; DOI=10.1093/molbev/msg065;
                                                                                                   100.0%; Score 33; DB 2; Length 47; 40.0%; Pred. No. 5.5e+02; tive 6; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 33; DB 2; Length 49; 40.0%; Pred. No. 5.7e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus licheniformis (strain DSM 13 / ATCC 14580).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=279010;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47 AA; 5106 MW; 8A53B1DCB6D7C951 CRC64;
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Last annotation update)
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InterPro; IPR010070; Cons_hypoth_TTM.
IIGRFAMs; IIGR01732; tiny_TM_bacill; 1.
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VG38 BPMD2
ID VG38 BPMD2 STANDARD;
AC 064229;
DT 15-DEC-1998 (Rel. 37, Created)
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25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
Hypothetical protein.
OrderedLocusNames=BL02399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QE2SA3 BACLD PRELIMINARY;
Q62SA3;
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FGYGGGCCGG 12
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13 FGAGRRICAG 22
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SEQUENCE 49 AA; 479
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Matches 4; Conserv
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0628A3 BAC
10 25 SA3
AC 0628A
AC 0628A
DT 25 SOC
DT 25 S
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Local Similarity
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Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                      Query Match
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   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alatroemeria hybrid cultivar 'Samora'.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Alstroemeriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Editiopterygii; Meopterygii; Teleostei; Buteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;

Trachinoidei; Ammodytidae; Ammodytes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wagetaff C., Malcolm P., Rafiq A., Leverentz M., Griffiths G., Thomas B., Stead A., Rogers H.; Programmed call death (FCD) processes begin extremely early in Alstroemeria petal senescence."; New Phytol. 160:49-59(2003).
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Pred. No. 5.8e+02;
6; Mismatches 0; Indels
   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Table 1 Careft J. M. Stagg R.M., Craft J.A.; Robertson F.B., McPhail M.E., Stagg R.M., Craft J.A.; Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases. -!- SIMILARITY: Belongs to the cytochrome P450 family. EMBL; AJ130768; CAA10203.1; -; mRNA. GO:0046872; F:metal ion binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rogers H.J.;
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AAS14409; CAD55820.1; -; mRNA.
InterPro; IRR03038; DAD.
Pfam; PF02109; DAD; 1.
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                                                                                                                                                                                                                                                                                                                                     05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 26, Last annotation update)
Cytochrome P450 1A (Fragment).
Name=CYP1A1;
                                                                                                                                                                                                                                                                              50 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54 AA.
6; Mismatches
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                                                                                                                                                                                                                                                                              PRT;
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Name=dad1;
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Q9YH75;
                                                                                                                                                                                                                                                                              Q70WU5_9LILI PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Conservative
4; Conservative
                                                       1 FXXGXXXCXG 10
                                                                                           |::|::|:|
31 FGVGRRRCVG 40
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8 FLSGVLSCVG 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rissum=Petal;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alstroemeria
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NON TER
SEQUENCE
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OVOWUS 9LI
OD OVOWUS
DT 05-JU
Matches
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NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=1P32953 / Serotype 1;
PubMed=15358858; DoI=10.1073/pnas.0404012101;
Chain P.S.G., Carniel B., Larimer F.W., Lamerdin J., Stoutland P.O.,
Regala W.M., Georgescu A.M., Vergez L.M., Land M.L., Motin V.L.,
Brubaker R.R., Fowler J., Hinnebusch J., Marceau M., Medigue C.,
Simonet M., Chenal-Francisque B., Dacheux D., Elliott J.M.,
Derbise A., Hauser L.J., Garcia B.;
"Insights into the evolution of Yersinia peetis through whole-genome comparison with Yersinia pseudotuberculosis.";
Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831(2004).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Putative phage minor tail protein.
OrderedLocusNames=YPTBL705;
Yershinia pseudotuberculosis.
Bacteria, Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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Pred. No. 6.4e+02;
                                                                                             0; Indels
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SEQUENCE 55 AA; 6624 MW; D20E1ADD3FF2F29D CRC64;
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Last annotation update)
GO; GO:0004497; F:monooxygenase activity; IEA. GO; GO:0006118; P:electron transport; IEA.
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                  GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR001128; Cytochrome P450.
InterPro; IPR002401; EP4501.
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01-MAY-1999 (TrEMBLrel. 10, Las
01-MAR-2004 (TrEMBLrel. 26, Las
Cytochrome P450 1A (Fragment).
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ID Q9YH73 SCOMX PRELIMINARY;
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QGGBRS, YERPS
ID QGGBRS_YERPS PRELIMINARY;
AC QGGBRS;
                                                                                                                                                                                                                                                                                                                                                           4; Conservative
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FGLGKRRCIG 44
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24 FVLGHTHCWG 33
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[1] — NUCLEOTIDE SEQUENCE. MUCLEOTIDE SEQUENCE. MEDILINE=85107103; PubWed=3968537; Takeshima H., Inokoshi J., Namiki M., Shimada J., Omura S.; "Structural analysis of the gene coding for hepatitis B virus surface
10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Cytochrome P450 (Fragment).
Musca domestica (House fly).
Bukaryota; Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Bidopterygota; Diptera; Brachycera; Muscomorpha; Muscoidea;
Muscaides; Musca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 33; DB 2; Length 64; Pred. No. 7.3e+02; 6; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 64;
                                                                                                                                                                                                                                                                                  Ma C.X., Qiu X.H., Li M., He F.Q., Liu H.X.; Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
-- SIMLIARITY: Belbings to the cytochrome P450 family.
EMBL; AY960134; AAX54685.1; -; mRNA.
GO; GO:0004497; F:monooxygenase activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR001128; Cytochrome P450.
PROSITE; PS00086; CYTOCHROME P450; UNKNOWN 1.
Heme: Iron; Metal-binding; Monooxygenase; Öxidoreductase.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
Surface antigen (HB&Ag).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 33; DB 2;
40.0%; Pred. No. 7.3e+02;
tive 6; Mismatches 0;
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J. Gen. Virol. 66:195-200(1985).

EMBL; M33808; AAA45500.1; -; mRNA.
GO; GO:015032; P:Viral life cycle; IEA.
InterPro; IPR000349; Hepvir surfAg.
PANTHER; PTHR10832; Hepvir surfAg.
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Q81160;
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Q9Y087;
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FGEGPRNCIG 11
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41 FLGGAPTCLG
                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best_Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Q9Y087 GLO
ID Q9Y08
AC Q9Y08
DT 01-NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
             8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,
Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Kawai J.,
Hayashizaki Y., Shinozaki K.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AK11829; BAC42917.1; -; mRNA.
GO; GO:0046872; F:metal ion binding; IEA.
GO; GO:006447; F:mocoxygenase activity; IEA.
InterPro; IPR001128; Cycokrome_P450.
Pfam; PF00067; p450; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein At1957750/T8123_21.
Name=At1957750/T8123_21;
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eud
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 33; DB 2; Length 60; 40.0%; Pred. No. 6.9e+02; ive 6; Mismatches 0; Indels
                                                                                                        Robertson F.E., McPhail M.E., Stagg R.M., Craft J.A.; Submitted (NOV-1998) to the EMBL/GenBank/DDBJ database-
-- SIMILARITY: Belongs to the cytochrome P450 family.
EMBL; AJ130770; CAA10205.1; -; mRNA.
GO; GO:0046872; F:metal ion binding; IEA.
GO; GO:0004497; F:moroxygenase activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR001128; Cytochrome_P450.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 AA; 6988 MW; 5379CF03ED02A142 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00086; CYTOCHROME P450; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                             63 AA.
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QS8F97 MUSDO .
ID Q58F97 MUSDO PRELIMINARY;
AC QS8F97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QBGXD1 ARATH PRELIMINARY;
QBGXD1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 40.0
Matches 4; Conservative
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41 FGLGKRRCIG 50
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                                                             NUCLEOTIDE SEQUENCE.
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          NCBI_TaxID=52904;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=3702;
                                                                                           TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical
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Q8GXD1 ARA
DG Q8GXD1
AC Q8GXD
AC Q8GXD
DT 01-MA
DE RNA
RNA NGEI
RNA SEKI
RNA HAYBA
RNA SEKI
RNA SEKI
RNA HAYBA
RNA SEKI
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Query Match
Best Local Similarity
Matches 4; Conserv
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                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                   0915Y3
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     8548888F8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLECTIDE SEQUENCE.

MUCLINES BRA17765; PubMed=2837739;
Thompson D.V.,
Hooykaas P.J.;
Hooykaas P.J.;
Malchers L.S., Idler K.B., Shilpercort R.A.,
Hooykaas P.J.;
Mallysis of the complete nucleotide sequence of the Agrobacterium
tumefaciens virs operon.";
Mucleic Acids Res. 16:4621-4636(1988).
                                                             Globodera rostochiensis (Golden nematode worm).
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
Tylenchoidea; Heteroderidae; Heteroderinae; Globodera.
NCBI_TaxID=31243;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 33; DB 2; Length 66; 40.0%; Pred. No. 7.5e+02; tive 6; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schrammeijer B.; Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                Oin L., Schots A., Smant G., Bakker J., Helder J., Submitted (FRB-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AJ13199; CAB45527.1; -; mRNA. HSSP; P0S091; 1002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (NOV-1990) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- SIMILARITY: Belongs to the cytochrome P450 family.
                                                                                                                                                                                                                                                                                                                                                                               66 66 AA; 7168 MW; FAAFAF2FA8F831A8 CRC64;
(TrEMBLrel. 12, Last sequence update) (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001 (TYEMBLrel. 16, Created)
01-MAR-2001 (TYEMBLrel. 16, Last sequence update)
01-MAR-2004 (TYEMBLrel. 26, Last annotation update)
P-450-type monooxygenase (Fragment).
                                                                                                                                                                                                                                           GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
Intervo; IRR002086; Aldehyd dehydrog.
Pfam: PF00171; Aldedh; I.
PROSITE; PS00070; ALDEHYDE DEHYDR CYS; I.
PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; I.
                                  Aldehyde dehydrogenase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Exp. Bot. 347:1167-1169(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Agrobacterium tumefaciens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9F452 9RHIZ PRELIMINARY,
Q9F452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 FXXGXXXCXG 10
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FNQGQCCCAG 54
                                                                                                                                                 NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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                                                                                                                                                                                                                                                                                                                                                Oxidoreductase,
 01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thompson D.;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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097452 9RH
10 01-MA
DT 01-MA
RN (1]
RN MCLIE
RN (2)
RN (3)
RN (4)
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Gaps
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EMBL; X06826; CAC15160.1; -; Genomic_DNA.
HSSP; Q91.142; 1GWI.
GO; GO:0004497; F:monooxygenase activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR001128; Cytochrome_P450.
HCSTIE; PS00086; CYTOCHROWE_P450.
Heme; Iron; Metal-binding; Monooxygenase; Öxidoreductase; Plasmid.
NON_TER.
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Pseudomonadaceae; Pseudomonas.
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Diptera; Diptera; Chironomidae; Chironominae; Chironomus.

NCBI_TaxID=7153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 33; DB 2; Length 66; 40.0%; Pred: No. 7.5e+02; ive 6; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=ATCC 15692 / PAO1;
MEDLINE-20437337; PubMed=10984043; DOI=10.1038/35023079;
                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                          66 AA; 7329 MW; 824AAC9FE080AADF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome, Hypothetical protein.
SEQUENCE 66 AA; 7030 MW; 67FFE339CDF97712 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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01-MAY-2000 (TYEWBLrel. 13, Last sequence update)
01-JUN-2003 (TYEWBLrel. 24, Last annotation update)
CE75-E75A ecdysteroid receptor homolog (Fragment).
                                                                                                                                                                                                                                                       100.0%; Score 33; DB 2;
40.0%; Pred. No. 7.5e+02;
tive 6; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE004492; AAG03942.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2004 (TrEMBLrel. 26, Hypothetical protein. OrderedLocusNames=PR0553;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QPISY3 PSEAE PRELIMINARY;
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Best Local Similarity 40.v-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OFTX04_CHITE PRELIMINARY;
                                                                                                                                                                                                                                                                                                         4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 406:959-964 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             opportunistic pathogen.
                                                                                                                                                                                                                                                                                                                                                           1 FXXGXXXCXG 10
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FGSGPHHCPG 17
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11 FCLGLAACSG 20
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Length 68;

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NUCLEOTIDE SEQUENCE.
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Best Local Similarity
Matches 4; Conserv
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                                   Query Match
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                                                                                                                                                                                                                                                                                              RSPP; P03372; IHCQ.

SMR; Q9TX04; 1-67.

GO; GO:005634; C:nucleus; IEA.

GO; GO:0006819; F:ligand-dependent nuclear receptor activity; IEA.

GO; GO:0004879; F:ligand-dependent nuclear receptor activity; IEA.

GO; GO:00063700; F:ranscription factor activity; IEA.

GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

RO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

RO; GO:0006350; P:regulation; IEA.

RO; GO:0006350; P:regulation; IEA.

RO; GO:0065350; P:ranscription;

RICEPTO; IPR001624; VIt_Creceptor.

RR PRINTS; PR00165; ZF-C4; 1.

RR PRINTS; PR00399; ZnF_C4; 1.

RR PRINTS; PR00399; ZnF_C4; 1.

RR PROSTIE; PR00399; ZnF_C4; 1.

RR PROSTIE; PR00399; ZnF_C4; 1.

RR PROSTIE; PR00390; ZnF_C4; 1.

RR PROSTIE; PR00390; ZnF_C4; 1.

RR PROSTIE; PR00390; ZnF_C4; 1.

RR PROSTIE; PR00391; Mctal-binding; Nuclear protein; Receptor; Transcription;

Transcription regulation; Zinc; Zinc-finger.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=95251674; PubMed=7733943; Seree E.M. Botto F., Pisano P., Lechevalier E., Desobry A., Barra Y.; "Evidence for the existence of two human CYP2E1 cDNAs using different
                                                                                                                               "Immunological studies on the developmental and chromosomal distribution of ecdysteroid receptor protein in Chironomus tentans."; Arch. Insect Biochem. Physiol. 30:95-114(1995).
-!- SUBCELULAR LOCATION: Nuclear (By similarity).
-!- SIMILARITY: Belongs to the nuclear hormone receptor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
NUCLEOTIDE SEQUENCE.
MEDLINE=96088569; PubMed=7579577;
Wegmann I.S., Quack S., Spindler K.D., Dorsch-Hasler K., Vogtli M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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Biochem. Blophys. Res. Commun. 209:717-722(1995).
-! SIMILARITY: Belongs to the cytochrome P450 family.
EMBL; S77873, AAD14267.1; -; mRNA.
HSSP; P11712; 10G2.
GO; GO:0004497; F:moncoxygenase activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR00128; Cytochrome_P450.
InterPro; IPR00128; Cytochrome_P450.
PEmi; PF00067; P45051.
PRINTS; PR00463; E84501.
PROSITE; PS00086; CYTOCHROME_P450; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 AA; 7822 MW; 42558F74AD1AE611 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYP2El protein (Fragment).
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016868 HUM
016868 HUM
016869 HUM
01-NO
01 01-NO
01 01-NO
01 01-NO
02 NAMENDER
03 NAMEDIA
04 NO
05 
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MEDLINE-22737999; Pubbled=12853948; DOI=10.1038/nature01782;
RA Hillier L.W., Fulton R.S., Fulton L.A., Graves T.A., Pepin K.H.,
RA Hagner-McParson C., Layman D., Maas J., Jaeger S., Walker R.,
Rylie K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,
Rylie K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,
Rylie K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,
Rylie K., Sekhon M., Du H., Man W. B., Cordes M., Du H.,
RA Sun H., Edwards J., Bradshaw-Cordum H., Ali J., Andrews S., Isak A.,
Vanbrunt A., Nguyen C., Du F., Lamar B., Courtney L., Kalicki J.,
RA Caersky P., Bielicki L., Scott K., Holmes A., Harkins R., Harris A.,
Rozlowicz-Reilly A., Leonard S., Rohlfing T., Rock S.M.,
Rozlowicz-Reilly A., Leonard S., Rohlfing T., Rock S.M.,
R. Ain-Wollam A.-M., Abbott A., Minx P., Maupin R., Strowmatt C.,
RA Latreille P., Miller N., Johnson D., Murray J., Woessner J.P.,
RA Hickenbotham M.T., Eldred J., Williams D., Bedell J.A., Mardis E.R.,
Rifton S.W., Chissoe S.L., Marra M.A., Raymond C., Haugen E.,
R. Simms E., Levy R., Clendenning J., Kaul R., Kent W.J., Purey T.S.,
RA Bailey M.A., Portnoy M.E., Torrents D., Chinwalla A.T., Gish W.R.,
Rady S.R., McPherson J.D., Olson M.V., Eichler E.E., Green E.D.,
R. Wilson R.K., St. K.K.;
R. Wereston R.H., Wilson R.K.;
R. Wenn R.H., St. Reibler R.K.;
R. Wereston R.H., Wilson R.K.;
R. Wereston R.H., Wilson R.K.;
R. Wenn R.H., Reibler R.K.;
R. Wenn R.L., Reibler R.K.;
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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Score 33; DB 2; Lengard No. 7.8e+02; O; Indels
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Pred. No. 7.8e+02;
6; Mismatches 0; Indels
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EMBL; AC011738; AAS02010.1; -; Genomic_DNA.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LaPlant Y., Stoneking T.;
to the EMBL/GenBank/DDBJ databases
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Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                      100.0%; Score 33; UD 40.0%; Pred. No. 7.8e tive 6; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUL-2004 (TrEMBLrel. 27, Last seque: 05-JUL-2004 (TrEMBLrel. 27, Last annot Hypothetical protein STK17A (Fragment) Name-STK17A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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                                                                                                                                                                                                                                                                                                                                                                                               RESULT 31
Q75MK4 HUMAN
ID Q75MK4_HUMAN PRELIMINARY;
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                                                                                                     Best Local Similarity 40.0
Matches 4; Conservative
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5 FSAGKRVCAG 14
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68 AA

64

55 PQDGYSLCPG

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Yeo A.E., Orito E., Ito K., Hirashima N., Ide T., Sata M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . Score 33; DB 2; Length 68
Pred. No. 7.8e+02;
6; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                   Tanaka Y., Yeo A.E., Orito E., Ito K., Hirashima N., Ide Mizokami M.;

Mizokami M.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AB111113; BAD02901.1; -; Genomic DNA.
GO; GO:0016032; P:viral life cycle; IEĀ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 AA; 7163 MW; 7351D6EAA55E17AD CRC64;
                                                                                                                                                                                                                        Viruses, Retro-transcribing viruses; Hepadnaviridae,
Orthohepadnavirus.
                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000349; Hepvir_surfAg. PANTHER; PTHR10832; Hepvir_surfAg; 1.
                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
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                                                                                   05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                  Q76BJ9 HPBV0 PRELIMINARY;
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Best Local Similarity 40.0
Matches 4; Conservative
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Matches 4; Conservative
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41 FLGGAPACPG 50
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Hepatitis B virus.
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                                                                                                                                                                                                 Hepatitis B virus.
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                                                                                                                                                                                                                                                                                     NCBI_TaxID=10407;
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                                                                                                                                                                       HBs antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antigen.
SEQUENCE
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Q7THR3 HPBV0
        276BJ9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Viridiplantae, Střeptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, rosides, euroside I; Rosales, Rosaceae, Rosoideae, Fragaria.
                                                                                                                                                                                                                                                                                  Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
                                                                                                                                                                                                                                                                                                                                                                                          Lohr J.E., Chen F., Hill R.T.;
"Genomic Analysis of Bacteriophage PhiJL001: Insights into Its
Interaction with a Sponge-Associated Alpha-Proteobacterium.";
Appl. Environ. Microbiol. 71:1598-1609(2005).
EMBL; AX576273; AA7659531.1; -; Genomic DNA.
SEQUENCE 68 AA; 7666 MW; 78D629C164309F70 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 33; DB 2; Length 68; 40.0%; Pred. No. 7.8e+02; ive 6; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Balogh A., Koncz T., Kiss E., Heszky L.E.;
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: Belongs to the cytochrome P450 family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68 AA; 7416 MW; 9D232752B90EB217 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                             Created)
Last sequence update)
Last annotation update)
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GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR001128; Cytochrome_P450.
InterPro; IPR0012401; EP4501.
InterPro; IPR005401; EP4501.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AY633994; AAT46620.1; -; mRNA.
GO; GO:0046872; F:metal ion binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00067; p450; 1.
PRINTS; PR00463; EP4501.
PROSITE; PS00086; CYTOCHROME P450; 1.
                                                         PRT;
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                                                                                                        10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30,
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QGGVFO;
                                                         OSDNSO_9CAUD PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 40.0
Matches 4; Conservative
                                                                                                                                                                                                                        ORFNames=JL001p55;
Bacteriophage phi JL001.
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FGAGRRICPG 15
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RESULT 32
0SDNSO 9CA
1D 0SDNS
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DT 10-MP
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DT 10-MP
DT 10-MP
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Pred. No. 7.8e+02;
Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                       68 AA; 7220 MW; 668BE6EAA545161D CRC64;
                                                                                                                                   Viruses; Retro-transcribing viruses; Hepadnaviridae;
                                                       Last sequence update)
Last annotation update)
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68 AA
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6; Mismatches
                                     Created)
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PANTHER; PTHR10832; Hepvir surfAg;
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Q80GT7_HPBV0
ID Q80GT7_HPBV0 PRELIMINARY;
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Dong J., Cheng J., Wang Q.H., Shi S.S., Hong Y., Huangfu J.K.,
Wang G., Li L., Si C.W.;
"The study on quasispecies of hepatitis B virus: reverse transcriptase
region in polymerase gas an example.";
Jie Pang Jun Yi Xue Za Zhi 26:823-825(2002).
EMBL, AF335734; AAK19537.1; -; Genomic_DNA.
GO; GO:0019031; C:viral life cycle; IEA.
InterPro; IPR000349; Hepvir_surfAg: 1.
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"The study on quasispecies of hepatitis b virus: reverse transcriptase region in polymerase gene as an example.";
Ping Tu Hsueh Pao 17:270-272(2001).
                                                                                                                                                                                                                                     Vaishall C., Acharya S.K., Panda S.K.; "Cryptic Hepatitis B virus infection: analysis of the complete genomic sequence of HBV from nine patients with seronegative viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=B11;

Dong J., Cheng J., Huangfu J.K., Hong Y., Wang G., Chen C.G., Li L. Ahang L.X., Chen J.M.;

"Theng L.X., Chen J.M.;

"The preliminary study on individually characterized quasispecies hepatitis B virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dong J., Cheng J., Wang Q.H., Shi S.S., Hong Y., Huangfu J.K., Wang G., Li L., Si C.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 33; DB 2; Length 68; 40.0%; Pred. No. 7.8e+02; Live 6; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                      hepatitis.";
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AYIGI151, AAO12668.1; -; Genomic DNA.
GO; GO:0016032; P:viral life cycle; IEĀ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 AA; 7295 MW; D3DF16EF59276A8B CRC64;
                                                                                                Viruses, Retro-transcribing viruses, Hepadnaviridae,
Orthohepadnavirus.
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000349; Hepvir surfAg.
PANTHER; PTHR10832; Hepvir surfAg; 1.
Pfam; PF00695; vMSA; 1.
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                                                       Clone S6.2, complete genome.
Hepatitis B virus.
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Q991LO HPBVO PRELIMINARY;
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Best Local Similarity 40.0
Matches 4; Conservative
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41 FLGGTTVCLG 50
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STRAIN=B11;
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                                                                                                                                                                NCBI_TaxID=10407;
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SEQUENCE
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01-MAR-2003 (TYEWBLrel. 23, Last sequence update)
01-MAY-2005 (TYEWBLrel. 30, Last annotation update)
Clone 56.5, complete genome (Clone S6.7, complete genome).
Hepatitis B virus.
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Vadiblal C., Acharya S.K., Panda S.K.;
"Cryathic Hepatitis B virus infection: analysis of the compective Hepatitis B virus infection: analysis of the compequence of HBV from nine patients with seronegative viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 33; DB 2; Length 68;
Pred. No. 7.8e+02;
6; Mismatches 0; Indels
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Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY161154; AA012677.1; -; Genomic_DNA.
EMBL; AY161155; AA012688.1; -; Genomic_DNA.
GO; GO:0016032; P:viral life cycle; IEĀ.
                                                                                                                                                                                                                                                                                                                        Lin X., Zhenz,
Lin X., Zhenz,
Lin X., Zhenz,
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AY206393; AAP06652.1; -; Genomic DNA.
GO, GO.0010632; Peviral life cycle; IEĀ.
InterPro; IPR000349; Hepvir surfAg.
PANTHER; PTHR10832; Hepvir surfAg; 1.
Pfam; PF00695; vMSA; 1.
                01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Truncated S protein.
Hepatitis B virus.
Hepatitis B virus.
Orthohepadnavirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 AA; 7235 MW; 777BE6EAB994DB1D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses, Retro-transcribing viruses; Hepadnaviridae,
Orthohepadnavirus.
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PANTHER; PTHR10832; Hepvir surfAg; 1.
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QBB4D4;
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QBAZ65_HPBVO PRELIMINARY;
QBAZ65;
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Best Local Similarity 40...
4; Conservative
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41 FLGGTTVCLG 50
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41 FLGGAPTCPG 50
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                           STRAIN=FMU022;
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SEQUENCE
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Q8B4D4 HPB
ID Q8B4D
AC Q8B4D
DT 01-MA
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RESULT 37
QBAZ65 HPB
QBAZ65 HPB
QBAZ6
AC QBAZ6
DT 01-MA
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Maucell E., Bonneau L., Fischer C., Ozouf-Costaz C., Bernot A., Maucell E., Bonneau L., Fischer C., Ozouf-Costaz C., Bernot A., Nicade D., Jeffe D., Fisher S., Lutfalla G., Dossat C., Sequrens B., Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S., Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B., Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V., Equand C., Duprat S., Brottier P., Poulain J., De Berardinis V., Parra G., Lardier G., Chapple C., McKernan K.J., McSwan P., Bosak S., Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J., Lindbad-Toh K., Birren B., Nubbaum C., Kahn D., Robinson-Rechavi M., Laudet V., Schachter V., Weissenbach J., Roest Crollius H., Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.; Genome duplication in the teleost fish Tetraodon nigroviridis reveals
  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, etrinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei, Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes, Tetraodontidae, Tetraodontiformes, Tetraodontidae, Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ueda K., Yamashita A., Ishikawa J., Shimada M., Watsuji T., Morimura K., Ikeda H., Hattori M., Beppu T.; "Genome sequence of Symbiobacterium thermophilum, an uncultivable bacterium that depends on microbial commensalism."; Nucleic Acids Res. 32.4937-4944(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nitted (FEB-2004) to the EMBL/GenBank/DDBJ databases. CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 33; DB 2; Length 69; red. No. 7.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genoscope, Whitehead Institute Centre for Genome Research,
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 68;
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Heme; Iron; Membrane; Metal-binding; Monooxygenase; (
SEQUENCE 68 AA; 7920 MW; E367B1591080F9B6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete proteome; Hypothetical protein.
SEQUENCE 69 AA; 7618 MW; 50F6B384E1DF1C3F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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Pred. No. 7.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RMBL; CAAE01014590; CAG00100.1; -; Genomic_DNA.
InterPro; IPR001128; Cytochrome_P450.
InterPro; IPR002401; EP4501.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Symbiobacterium thermophilum.
Bacteria; Actinobacteria; Symbiobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=15383646; DOI=10.1093/nar/gkh830;
                                                                                                                                                                                                                                                                                                                                                                                                                    the early vertebrate proto-karyotype.";
Nature 431:946-957(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No.
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40.0%; E
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40.0%; F
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QE7NC4 SYMTH PRELIMINARY;
Q67NC4;
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es 4; Conservative
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                                                                                                                              NUCLEOTIDE SEQUENCE,
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Matches 4, Conserv
                                                                                  NCBI_TaxID=99883;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
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Matches
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Wang G., Li L., Si C.W.;
"The study on quasispecies of hepatitis B virus: reverse transcriptase
                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dong J., Cheng J., Huangfu J.K., Hong Y., Wang G., Chen C.G., Li L., Zhang L.X., Chen J.M., "The preliminary study on individually characterized quasispecies of hepatitis B virus.";
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Pred. No. 7.8e+02;
6; Mismatches 0, Indels
                                                                 Length 68;
                                                                                                      0; Indels
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome 14 SCRF14590, whole genome shotgun sequence.
ORFNames=GSTENG00018412001;
                     A59A071AB6BA159D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lope protein.
AA; 7220 MW; 669A071AA8752B1D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; Retro-transcribing viruses; Hepadnaviridae;
Orthohepadnavirus.
                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                          100.0%; Score 33; DB 2;
40.0%; Pred. No. 7.8e+02;
iive 6; Mismatches 0
                                                                                                                                                                                                                                                                                             68 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        region in polymerase gene as an example.";
Jie Fang Jun Yi Xue Za Zhi 26:823-825(2002)
EMBL, AF129859; AAG48739.1; -; Genomic_DNA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0016032; P:viral life cycle; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fang Jun Yi Xue Za Zhi 27:119-121 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000349; Hepvir_surfAg.
PANTHER; PTHR10832; Hepvir_surfAg; 1.
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                                                                                                                                                                                                                                                                                                                                      Created)
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Antigen; Envelope protein.
SEQUENCE 68 AA; 7182 MW;
                                                                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40.08;
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Q9DKQ0;
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Q4SGY2;
                                                                                                      4; Conservative
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41 FLGGASTCPG 50
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FLGGAPTCPG 50
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Best Local Similarity
                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis B virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaXID=10407;
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SEQUENCE 69
                                                            Query Match
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RESULT 40
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RESULT 41 Q4SGY2 TET 1D Q4SGY D7 13-SE DT 13-SE DT 13-SE DT 13-SE DF 13-SE DF 08-NOW GN ORFIVA

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MEDLINE=22676373; PubMed=12791874;
DOI=±0.1128/JCM.41.6.25169-2514.2003;
Antonsson A., Karanfilovska S., Lindqvist P.G., Hansson B.G.;
"General acquistiton of human papillomavirus infections of skin occurs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=MCS6 (Serogroup B; MEDINIO307; DOI=10.1126/science.287.5459.1809; MEDINE=20175755; PubMed=10710307; DOI=10.1126/science.287.5459.1809; Tettelin H., Saunders N.J., Heidelberg J.F., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Hickey B.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Hickey B.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T.M., Ciecko A., Parksey D.S., Blair B., Cotton M.D., Utterback T.R., Khouri H.M., Qin H., Vamathevan J.J., Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon B.R., Rappuoli R., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete genome sequence of Neisseria meningitidis serogroup B strain
                                                                                                                                                                                                                                                                                                                                                                             Neisseria meningitidis (serogroup B).
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
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                                  Length 71;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete proteome; Hypothetical protein.
SEQUENCE 71 AA; 8091 MW; 4A25DBB87621F66B CRC64;
71 AA; 8104 MW; 50EE1A62D021F67E CRC64;
  50kbi...
Score 33; DB 2; Len:
No. 8.1e+02;
0;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                        01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UJUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein.
OrderedLocusNames=NMB2131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 33; DB 2;
Pred. No. 8.1e+02;
5; Mismatches 0;
                                                                                                                                                                                                                                                      71 AA
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EMBL, AE002098; AAF42439.1; -; Genomic_DNA.
PIR; D81003; D81003.
                                                                            6; Mismatches
                                                        Pred. No.
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40.0%; P
                                    100.08;
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                                                                                                                                                                                                                                                      Q9JXB9_NEIMB PRELIMINARY;
                                                                          4; Conservative
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2 FKLGVYTCLG 11
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FKLGVYACLG
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  SEQUENCE
                                        Query Match
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                                                                            Matches
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MEDLINE=2022556; PubMed=10761919; DOI=10.1038/35006655;
Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.M.,
Riee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
Jagels K., Leather S., Moule S., Mungall K.L., Quail M.A.,
Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
Whitchead S., Spratt B.G., Barrell B.G.; strain of Neisseria
meningitidis 22491.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=96417083; PubMed=8819874; DOI=10.1104/pp.110.3.1035; Frank M.R., Deyneka J.M., Schuler M.A.; "Cloning of wound-induced cytochrome P450 monooxygenases expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                            Pisum sativum (Garden pea).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, eudicotyledons, core eudicots, rosids,
euroalda I, Fabales, Fabaccae, Papilionoideae, Vicieae, Pisum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Pisum sativum clone MFRTPCR62 wound-inducible cytochrome P450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neisseria meningitidis (serogroup A).
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
NCBI_TaxID=65699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 33; DB 2; Length 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70 AA; 7952 MW; F8E8E7CA1752CA23 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-007-2000 (TrEMBLrel. 15, Created)
01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-078-2003 (TrEMBLrel. 24, Last annotation update)
Putative integral membrane protein.
OrderedLocusNames=NMA0300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 8e+02;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 404:502-506(2000).
EMBL; AL162752; CAB83605.1; -; Genomic_DNA.
PIR; D82025; D82025.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Flant Physiol. 110:1035-1046 (1996).
EMBL; U29335; AAC49190.1; -; mRNA.
PIR; T06525; T06525.
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR001128; Cytochrome_P450.
                                                                                                                                                           5
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                                                                                                                                                                                                 Created)
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                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9JWM3 NEIMA PRELIMINARY;
Q9JWM3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Conservative
                                                                                                                                       16 PEA
Q40986 PEA PRELIMINARY;
Q40986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 FXXGXXXCXG 10
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FALGDASCSG 58
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6 FQAGPRVCLG 15
                      1 FXXGXXXCXG
                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=3888;
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                                                                                                                   RESULT 43
040986 PBA
D40986 PBA
D5 04098
D6 04098
D7 01-NO
D7 01-NO
D7 01-NO
D8 04098
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WICLECTIDE SEQUENCE.
MEDIJINE=22695342; PubMed=12810883; DOJ=10.1099/vir.0.18836-0;
MEDIJINE=22695342; PubMed=12810883; DOJ=10.1099/vir.0.18836-0;
Antonsson A., Erfurt C., Hazard K., Holmgren V., Simon M., Kataoka A.,
Hossain S., Hakangard C., Hansson B.G.;
"Prevalence and type spectrum of human papillomaviruses in healthy
skin samples collected in three continents.";
Gen. Virol. 84:1881-1886 (2003).
EMBL; AFS42100; AAN28675.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-22326806; PubMed=12438579;
DOI=10.1128/JVI.76.24.12537-12542.2002;
Antonsson A., Hansson B.G.;
"Healthy skin of many animal species harbors papillomaviruses which are closely related to their human counterparts.";
J. Virol. 76:12537-12542(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 33; DB 2; Length 72; 40.0%; Pred. No. 8.2e+02; ive 6; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 33; DB 2; Lengtn ,2
Pred. No. 8.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chimpanzee papillomavirus.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
unclassified Papillomaviridae; primate papillomaviruses.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae; unclassified Papillomaviridae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72 AA; 8182 MW; 6765F1107AC17C82 CRC64;
                                                                                                                                                                                                                                                                                                                                                             GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR002210; PV_capsid_L1.
Pfam; PF00500; Late protein L1; 1.
PRINTS; PR00865; HPVCAPSIDLI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 AA; 7953 MW; CEBAA6474A7F27D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GG); GO: 0019028; C: viral capsid; IEA.
GG); GO: 0005198; F: structural molecule activity; IEA.
INCEPEO; IFR002210; PV capsid_L1.
Pfan; PF00500; Late_protein_L1; 1.
PRINTS; PR00865; HPVCAPSIDLI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QBJSL4 9PAPI PRELIMINARY; PRT; 72 AA.
QBJSL4;
QBJSL4;
O1-OCT-2002 (TrEMBLrel. 22, Created)
O1-OCT-2003 (TrEMBLrel. 22, Last sequence update)
O1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Major capsid protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF488687; AAM97872.1; -; Genomic_DNA.
HSSP; Q9WPH4; 1DZL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProDom; PD000544; PV capsid_L1; 1.

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NON_TER 72 72
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Best Local Similarity 40.0
Matches 4; Conservative
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33 FIIGCTPCLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=203380;
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Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                             Length 71;
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Pred. No. 8.2e+02;
6; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Choi I., Moon K.D., Song I., Wiley J.W.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AF519545; AAN77120.1; -; Genomic_DNA.
SMR; QBIWZ9; 1-71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72 72
72 AA; 7993 MW; B61C9DEF13DBEC64 CRC64;
                                                                                                  DOST, WITTER, WITTER, CO. GO: 000519028; C. VITTER, GO; GO: 0005198; F: Structural molecule activity; IEA. INTER-PRO; IPRO02210; PV capsid_L1.
PERM: PRO0850; Late protein L1; 1.
PRINTS; PRO0865; HPVCAPSIDL1.
PRODOM: PD000544; PV_capsid_L1; 1.
                                                                                                                                                                                                                                                                                                                                   71 AA; 7998 MW; 8F7DDC13BB31393B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OBINES HUMAN PRELIMINARY; PRT; 72 AA.
081W29-
1-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Major capaid protein (Fragment).
Human papillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                          ; Score 33; DB 2;
Pred. No. 8.1e+02;
6; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypertension associated protein (Fragment). Home sapient (Human).
        J. Clin. Microbiol. 41:2509-2514 (2003).
EMBL; AF455145; AAL57872.1; -; Genomic_DNA.
HSSP; Q9WPH4; 1DZL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00320; WD40; 1.
PROSITE; PS00678; WD REPEATS 1; UNKNOWN 1.
PROSITE; PS50082; WD REPEATS 2; 1.
PROSITE; PS50294; WD REPEATS REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ensembl; ENSG0000111664; Homo sapiens.
InterPro; IFR001680; WD40.
Pfam; PF0040; WD40; 2.
Probom; PD000018; WD40; 1.
                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
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33 FIVGCAPCIG 42
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FPNGEAICTG 11
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Best Local Similarity
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081W22
AC 081W2
AC 081W2
DT 01-MA
DT 0
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Length 72;

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RESULT 50
0902R1,
0002R1,
0002R1,
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0000R1,
010-MAY-2000 (TERMELEI 13, Created)
010-MAY-2000 (TERMELEI 13, Last sequence update)
010-MAY-2000 (TERMELEI 13, Last sequence update)
010-MAY-2000 (TERMELEI 13, Last sequence update)
011-MAY-2000 (TERMELEI 13, Last sequence update)
020 Viruses; daDNA viruses, no RNA stage; Papillomaviridae;
031 Major capsid protein 11 (Fragment).
032 MCBL TAXID=1056;
033 MCBL TAXID=1056;
044 MCLEOTIDE SEQUENCE.
055 MCBL TAXID=1056;
056 MCBL TAXID=1056;
067 MCBL TAXID=1056;
068 MCLEOTIDE SEQUENCE.
069 MCLEOTIDE SEQUENCE.
070 MCBL TAXID=1056;
070 MCBL TAXID=10509;
070 MCBL TAXID=10
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Search completed: March 8, 2006, 11:23:55 Job time : 236 secs

8 8

## Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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us-10-751-235-10.rup

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein -	OM protein - protein search, using sw model
Run on:	Run on: March 7, 2006, 21:43:16 ; Search time 118.8 Seconds
	(without alignments)

US-10-751-235-10 122 1 LVAEVSEFLFGSGFAIAEGPLWTA 24 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2166443 segs, 705528306 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt\_05.80:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	Octbx7 arabidopsis			-			Q9k895 bacillus ha			Q8yjv8 anabaena sp		Q93vk5 arabidopsis		Q92gnl rickettsia	P58187 rickettsia	Q7p9k9 rickettsia	P58186 rickettsia		Q5kwe4 geobacillus		Q4tsr2 erythrobact		Q7m860 wolinella s	Q9hed9 neurospora		_	Q632t7 bacillus ce	Q92ci7 listeria in	Q720k8 listeria mo	Q8y7q2 listeria mo	Q4p0g2 ustilago ma
QI	Q6TBX7 ARATH	Q8RWV4_ARATH	Q9SCP8 ARATH	Q9AV27_ORYSA	SYFA BACSK	Q9CFC7_LACLA	SYFA BACHD	Q5FPI9_GLUOX	SYFA_GEOSL	Q8YJV8 ANASP	Q9C6S0_ARATH	Q93VK5 ARATH	QBNQS2 CORGL	LPXK_RICCN	LPXK_RICRI	Q7P9K9 RICSI	LPXK RICMO	Q4UNI1_RICFE	SYFA GEOKA	Q6MJ94_BDEBA	Q4TSR2 9SPHN	SYFA_THETN	Q7M860_WOLSU	Q9HED9_NEUCR	Q93H59 STRAW	Q6HCC7_BACHK	Q632T7 BACCZ	SYFA LISIN	SYFA_LISMF	SYFA_LISMO	Q4P0G2_USTMA
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& Query Match	100.0	100.0	6.7	90.5	46.7	45.9	45.9	45.5	45.1	45.1	•	44.3	43.0	N	42.6	42.6	42.6	42.6	42.6	42.2	42.2	41.8	41.8	41.8	41.8	41.0	41.0	41.0		41.0	41.0
Score	122	122	118	110	57	26	26	55.5		22	54	54	52.5	52	25	52	. 52	52	52	51.5	51.5	51	51	51	51	20	20	20	20	20	20
Result No.	1	7	n	4	Ŋ	9	7	80	O	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31

O5w270 serratia sp Q'wav9 bordetella Q'wav9 bordetella Q'wcq8 bacillus ha Q89pwl bradyrhizob Q5wn3 anopheles g Q5sj53 thermus the Q72jh5 thermus the Q72jh5 thermus the Q9kd24 bacillus ha Q28d39 archaeoglob P95970 sulfolobus Q6c217 yarrowia li Q9vvt2 drosophila Q7qit2 anopheles g	A.  update)  update)  lase.  ryophyta; Tracheophyta;  s; core eudicotyledons;  sae; Arabidopsis.  lose; Arabidopsis.  tof the cytochrome p450  lon-ring hydroxylation  150 family.  L.  cidoreductase;	Length 539; ; Indels 0; Gaps 0;	e) . ate)
50 41.0 670 2 Q5W270 9ENTR 50 41.0 718 2 Q7WAV9_BORPA 49.5 40.6 287 2 Q9KCQ8_BACHD 49.5 40.6 524 2 Q9KCQ8_BACHD 49 40.2 275 2 Q5TWN_ANGGA 49 40.2 275 2 Q5TWN_ANGGA 49 40.2 275 2 Q5TSJ3_THETB 49 40.2 275 2 Q7ZJH5 THETB 49 40.2 287 2 Q9KD24_BACHD 49 40.2 287 2 Q9KD24_BACHD 49 40.2 287 2 Q9KD24_BACHD 49 40.2 575 2 Q7ZJH5 THETB 49 40.2 575 2 Q7ZJH SYK GTFU 49 40.2 572 1 INDX1_DROME	ALIGNMENTS  RATH PRELIMINARY; PRT; 539 AA.  1004 (TrEMBLrel. 27, Created) 1004 (TrEMBLrel. 27, Last sequence updat 004 (TrEMBLrel. 27, Last sequence updat 004 (TrEMBLrel. 27, Last sequence updat ast carotenoid epsilon-ring hydroxylase is thaliana (Mouse-ear cress).  3; Viridiplantae; Streptophyta; Embryophyta; Magnoliophyta; eudicotyledons; eurosids II; Brassicales; Brassicacea; ID=3702;  DE SEQUENCE. 4709673; DOI=10.1073/pnas.2237237100; Musetti V.; Kim J.; Magallanes-Lundbachat is required for carotenoid epsilon-ti. Acad. Sci. U.S.A. 101:402-407(2004) LARITY: Belongs to the cytochrome P450 Haki is required for carotenoid epsilon-ti. Acad. Sci. U.S.A. 101:402-407(2004) LARITY: Belongs to the cytochrome P450 Haki P: Enconoxygenase activity; IEA. 004497; F: monooxygenase activity; IEA. 1PR00128; Cytochrome_P450.  FR00185; P450.  PR00463; EP450I.	ttch 100.0%; Score 122; DB 2; 21 Similarity 100.0%; Pred. No. 1.1e-09; 24; Conservative 0; Mismatches 0; IVAEVSEFLFGSGFAIAEGPLWTA 24	NT 2  QBRWV4_ARATH PRELIMINARY; PRT; 552 AA. QBRWV4; Q1UUN-2002 (TrEMBLrel. 21, Created) 01UUN-2002 (TrEMBLrel. 21, Last sequence update) 01-VUN-2004 (TrEMBLrel. 26, Last annotation update) Putative cytochrome P450 (Fragment).
₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩	RESULT 1  OGTBX7 ARATH  ID QGTBX7 AC OGTBX7 AC OGTBX7 AC OGTBX7 AC OGTBX7 AC OGTBX7 AC OGTBY AC OG OGTBY AC OG	Query Match Best Local Matches 2 Qy 1	RESULT 2 QBRWV4 ARATH ID QBRWV4 A AC QBRWV4 D D 01-UIN-2 DT 01-MAR-2 DT 01-MAR-2 DE PLEALIVE

us-10-751-235-10.rup

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InterPro; IPR001128; Cytochrome P450.
InterPro; IPR002401; EP4501.
Pfam; PF00067; p450; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          144 LVAEVSEFLFGSGFAIAEGPLWT 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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Q9AV27; Q7XCI2;
                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                     PRINTS; PR00463; EP450I.
PRINTS; PR00385; P450.
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                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                     Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                        23,
                                                                                                                                                                                                                                                                               SEQUENCE
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Matches
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                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.

Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K.,
Davis R.W., Ecker J.R., Theologis A.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
--- SIMILARITY: Belongs to the cytochrome P450 family.
HSSP: P14779, 1JEZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Welchselgartner M., Mewes H.W., Lemcke K., Mayer K.F.X., Quetier F.,
                          Arabidopsis thaliana (Mouse-ear cress).
Makaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons, rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).
Strabtophyta, Tracheophyta, Embryophyta, Tracheophyta, Straptophyta, Spermatophyta, Magnoliophyta, eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae, Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 122; DB 2; Length 552; 100.0%; Pred. No. 1.2e-09; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00086; CYTOCHROME P450; UNKNOWN 1.
Heme; Iron; Metal-binding; Monooxygenase; Oxidoreductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            databases.
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Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases I-SIMILARITY: Belongs to the cytochrome P450 family. BENBL, AL12958; CAB64216.1; -; Genomic_DNA.
PIR; T46129; T46159.
PIRSP: P14779; JUPZ.
GO; GO: 0004872; F: metal ion binding; IEA.
GO; GO: 0004497; F: monooxygenase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 552 AA; 62073 MW; C23CF8498B5B8440 CRC64;
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01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Cytochrom P450-like protein.
Name=r4b2.00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0046872; F:metal ion binding; IEA.
GO; GO:0004497; F:monooxygenase activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR001128; Cytochrome_P450.
Pfam; PF00067; P450; 1.
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Q9SCP8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00463; EP450I.
PRINTS; PR00385; P450.
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Best Local Similarity
                                                                                                                            rosids; eurosids
NCBI_TaxID=3702;
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Gaps
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Buell C.R., Yuan Q., Ouyang S., Moffat K.S., Hill J.N., Burr P.C.,
Hsiao J., Zismann V., Pai G., Bowman C.L., Fujii C.Y., VanAken S.E.,
Bowman C.L., Craven B., Utterback T.K., Khalak H., Feldblyum T.V.,
Quackenbush J., White O., Salzberg S.L., Fraser C.M.,
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UJUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 29, Last annotation update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Putative cytochrome P450 monocxygenase.
ORFNames-OSUNBa0001014.16;
Oryza sativa (japonica cultivar-group).
Spermarophyta; Viridiplantes; Streptophyta; Embryophyta; Tracheophyta; Spermarophyta Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrarcioleae; Oryzeae; Oryzea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The Rice Chromosome 10 Sequencing Consortium, "In-depth view of structure, activity, and evolution of rice
                                                                                                                                                             Length 566;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN 1.
Heme; Iron; Metal-binding; Monooxygenase; Oxidoreductase;
Transmembrane.
SEQUENCE 584 AA; 64798 MW; 1A55160A532DCE83 CRC64;
PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
Heme; Iron; Metal-binding; Monooxygenase; Oxidoreductase;
                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases
                                                                                             566 AA; 63596 MW; B884E8996B1A4C7D CRC64;
                                                                                                                                                         96.7%; Score 118; DB 2; L
100.0%; Pred. No. 4.8e-09;
tive 0; Mismatches 0;
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Gramer, 1987,27; -..
GO; GO:0046872; F:metal ion binding; IEA.
GO; GO:0004497; F:menoxygenase activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR001128; Cytochrome_P450.
InterPro; IPR002401; EP4501.
PRINTS; PR00463; EP4501.
PRINTS; PR00463; EP4501.
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RESULT 5

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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                              MEDLINE=21235186; PubMed=11337471; DOI=10.1101/gr.GR-1697R;
Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K.,
Weissenbach J., Ehrlich S.D., Sorokin A.;
"The complete genome sequence of the lactic acid bacterium Lactococcus
lactis ssp. lactis IL1403.";
Genome Res. 11:731-753(2001).

EMBL; AE006386; AAK05652.1; -; Genomic_DNA.
                                                                                                                  Name=ypjP; OrderedLocusNames=LL1554; '
Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Pirmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000).
--- CATALYTIC ACTIVITY: ATP + L-phenylalanine + tRNA(Phe) = AMP + diphosphate + L-phenylalani-tRNA(Phe).
--- COFACTOR: Binds 2 magnesium ions per tetramer (By similarity).
--- SUBUNIT: Tetramer of two alpha and two beta chains (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 eimilarity).
-- SUBCELLULAR LOCATION: Cytoplasmic.
-- SUBCELLULAR Belongs to the class-II aminoacyl-tRNA synthetase
family. Phe-tRNA synthetase alpha chain type 1 subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C-125 / JCM 9153;
MEDLINE=20512582; PubMed=11058132; DOI=10.1093/nar/28.21.4317;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.
Puji P., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Length 324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBL_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               324 AA; 36603 MW; DBF47D6684EB259C CRC64;
                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
13-SEP-2005 (Rel. 48, Last sequence update)
Phenylalanyl-tRN synthetase alpha chain (EC 6.1
(Phenylalanine--tRNA ligase alpha chain (EC 8.1
Name-phes; OrderaedLocusNames=BH3111;
Bacillus halodurans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0016491; F:oxidoreductase activity; IEA. GO; GO:0006118; P:electron transport; IEA. GO; GO:0008152; P:metabolism; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 45.9%; Score 56; DB 1
Local Similarity 50.0%; Pred. No. 6.8;
hes 10; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           344 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000683; GFO/IDH/MocA N. InterPro; IPR004104; GFO_IDH_MocA_C.
                             Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF01408; GFO IDH MocA; 1.
Pfam; PF02894; GFO IDH MocA C; 1.
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                          01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; B86819; B86819.
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SEQUENCE 324 AA;
                                                                                                                                                                                    NCBI_TaxID=1360;
                                                                                              Oxidoreductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fuji Y., Hiram
Horikoshi K.;
                                                                                                                                                                                                                                                               STRAIN=IL1403
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Q9K895;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENEL outstation the Buropean Bioinformatics Institute. There are restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Takaki Y., Kageyama Y., Shimamura S., Suzuki H., Nishi S., Hatada Y.
Kawai S., Ito S., Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGRPAMS; TIGRO0468; pheS; 1.
PROSITE; PS50862; AA_TRNA_LIGASE II; 1.
Aminoacyl-tRNA synthetase; ATP-binding; Complete proteome; Ligase; Magnesium; Metal-binding; Nucleotide-binding; Protein biosynthesis.
METAL 256 258 Magnesium (By similarity).
SEQUENCE 344 AA; 38634 MW; 15F66E8B3556EICC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The complete genome sequence of the alkaliphilic Bacillus clausii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
-1- CATALYTIC ACTIVITY: ATP + L-phenylalanine + tRNA(Phe) = AMP + diphosphate + L-phenylalanyl-tRNA(Phe).
-1- COFACTOR: Binds 2 magnesium ions per tetramer (By similarity).
-1- SUBUNIT: Tetramer of two alpha and two beta chains (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- SIMILARITY: Belongs to the class-II aminoacyl-tRNA synthetase family. Phe-tRNA synthetase alpha chain type 1 subfamily.
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                             DB 2; Length 584;
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                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria, Pirmicutes, Bacillales, Bacillaceae, Bacillus
                                                                                                                                                                                                                                                                                                                         10-MAY-2005 (Rel. 47, Created)
10-MAY-2005 (Rel. 47, Last sequence update)
13-SEP-2005 (Rel. 48, Last amnotation update)
Phenylalanyl-tRNA synthetase alpha chain (BC 6.1.1.20)
(Phenylalanine--tRNA ligase alpha chain) (PheRS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
                                                                                                                                                                                                                                                                                     344 AA
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                     90.2%; Score 110; DE ilarity 95.7%; Pred. No. 8e-Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMBL; AP006627; BAD65215.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HAWAP; MP 00281; -; 1.
InterPro; IPR004186; Phe tRNA_synt_N.
InterPro; IPR004189; PheS.
InterPro; IPR002319; tRNA-synt_2d.
InterPro; IPR006195; tRNA_11gase_II.
PANTHER; PIRRILS38; tRNA-synt_2d; 1.
Pfam; PP02912; Phe tRNA-synt_2d; 1.
Pfam; PP01409; tRNA-synt_2d; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=pheS; OrderedLocusNames=ABC2680;
Bacillus clausii (strain KSM-K16).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gimilarity).
-1- SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                             152 LVAEVSEPLFGSGFAIAEGALWT 174
                                                                                                                  1 LVAEVSEFLFGSGFAIAEGPLWT 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113 WYTEIEFIFIGLGFSIGEGP 132
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                                                                                                                                                                                                                                                                                  STANDARD;
Query Match
Best Local Similarity
Loca 22; Conserve
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OSWEJS;
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Gaps

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Indels

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324 AA.

PRT;

OFCECT LACLA PRELIMINARY, OFCECT;

LACLA

RESULT 6 Q9CFC7 LA ID Q9CF AC Q9CF

Matches

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Local Similarity 75.0%;
ses 12; Conservative
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                      Matches
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use as long as its content is in no way modified and this statement is not
                                                                                                                  R HSSP; P27001; LUUC.

R HAMAP, MR 00201; -; 1.

R HAMAP, MR 00201; -; 1.

R InterPro; IPR004529; Phe LRNA_synt_N.

R InterPro; IPR004529; Phe S.

R InterPro; IPR006195; tRNA_synt_2d.

DR PE02912; Phe tRNA_synt_2d; 1.

DR PEm; PP02912; Phe tRNA_synt_2d; 1.

DR PEm; PF02912; Phe tRNA_synt_2d; 1.

DR PEm; PF02912; Phe LRNA_synt_2d; 1.

DR PGM; PF02912; Phe LRNA_synt_2d; 1.

DR PCSITE; PS50862; AA TRNA_LIGASE II; 1.

RAMINOACY1_KRNA synthetase; ATP-binding; Protein biosynthesis.

KW Magnesium; Metal-binding; Nucleotide-binding; Protein biosynthesis.

Magnesium; Metal-binding; Nucleotide-binding; Nucleotide-binding; Protein biosynthesis.

APPARAMENTATION SYNTHE STATE SECTION SAMINATION.

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APPARAMENTATION SYNTHESIS.
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Nat. Biotechnol. 23:195-200(2005).

-1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

EMBL, CPROGNOS; AAW61707.1; -; Genomic_DNA.

GO; GO:0016020; C:integral to membrane; IEA.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0016020; E:ranaporter activity; IEA.

GO; GO:000531; F:ranaporter activity; IEA.

GO; GO:0005415; F:transporter transport; IEA.

InterPro; IPRO01529; Sug_transporter.

InterPro; IPRO05829; Sug_transporter.

InterPro; IPRO05829; Sug_transporter.

InterPro; IPRO05829; Sug_transporter.

InterPro; IPRO05829; Sug_transporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gluconobacter oxydans (Gluconobacter suboxydans).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
Acetobacteraceae; Gluconobacter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45.9%; Score 56; DB 1; Length 344; 47.4%; Pred. No. 7.2; ive 4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfan; PF000A1, SUGAT LT; 1.
PRINTS; PR00171; SUGRTRNSPORT.
TIGRAPMS; TIGRO0879; PT; 1.
PROSITE; PS00216; SUGAR_TRANSPORT_1; UNKNOWN_1.
PROSITE; PS00217; SUGAR_TRANSPORT_2; Transport.
Complete proteome; Transmembrane; Transport.
SEQUENCE 470 AA; 49835 MW; ECBAC911C986E16C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        470 AA.
                                                                   EMBL; BA000004; BAB06830.1; -; Genomic_DNA.
PIR; G84038; G84038.
HSSP; P27001; 1JJC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=15665824; DOI=10.1038/nbt1062;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47.48;
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OrderedLocusNames=GOX1971;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QSFP19 GLUOX PRELIMINARY;
QSFP19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 47.4
Matches 9, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
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OSFP19 GL

OSFP 10-M

DT 10-M
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45.5%; Score 55.5; DB 2; Length 470;

Query Match

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PubMed=14671304; DOI=10.1126/science.1088727;

Methe B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C., Heidelberg J.F., Wu D., Wu W., Ward N.L., Beanan M.J., Dodson R.J., Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S., Gwinn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J., Gwinn M.L., Zafar N., White O., Tran B., Romero C., Forberger H.A., Weidman J.F., Khouri H.M., Feldblyum T.V., Utterback T.R., Van Aken S.E., Lovley D.R., Fraser C.M.;
"Genome of Geobacter sulfurreducens: metal reduction in subsurface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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TIGRFAMS, TIGROOAGS, pheS; 1.
PROSTER, PS50862; AA TRNA LIGASE II; 1.
Aminoacyl-tRNA synthetase; ATP-binding; Complete proteome; Ligase;
Aminoacyl-tRNA synthetase; ATP-binding; Complete protein biosynthesis.
Magnesium; Metal-binding; Nucleotide-binding; Protein biosynthesis.
Amagnesium; Metal-binding; Magnesium (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                        10-MAY-2005 (Rel. 47, Created)
10-MAY-2005 (Rel. 47, Last sequence update)
11-MAY-2005 (Rel. 48, Last annotation update)
Planglalanyl-tRNA synthetase alpha chain (EC 6.1.1.20)
(Phenylalanyl-tRNA synthetase alpha chain (PheRS).
Name-pheS; OrderedLocusNames-GSU1519;
Geobacter sulfurreducens.
Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales; Geobacteraceae; Geobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 302:1967-1969(2003).
-1- CATALYTIC ACTIVITY: ATP + L-phenylalanine + tRNA(Phe) = AMP + diphosphate + L-phenylalanyl-tRNA(Phe).
-1- COFACTOR: Binds 2 magnesium ions per tetramer (By similarity).
-1- COFACTOR: Binds 2 magnesium ions per tetramer (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similarity).
--- SUBCELLULAR LOCATION: Cytoplasmic.
--- SIMILARITY: Belongs to the class-II aminoacyl-tRNA synthetase family. Phe-tRNA synthetase alpha chain type 1 subfamily.
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                               Indels
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                                                                                                                                                                                                                                                                                                                                 339 AA.
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HSSP; P27001; 1B7Y.
Pred. No. 11;
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InterPro; IRR004188; Phe_tRNA_synt_N.
InterPro; IRR004189; PheS.
InterPro; IRR004189; PheS.
InterPro; IRR006195; tRNA_synt_2d.
InterPro; IRR06195; tRNA_ligase_II.
PANTHER; PTHRA1538; tRNA_synt_2d; 1.
Pfam; PP02912; Phe_tRNA_synt_N; 1.
Pfam; PP01409; tRNA_synt_N; 1.
                                                                                                                                                                                                                                                                                                                                 PRT;
                               1;
                                                                                                                                             365 LFVAGFAIGEGFLVWT 380
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                                                                                                9 LFGSGFAIAEGPL-WT
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Matches 9; Conserv
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Q74D00;
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Q93VKS_ARATH PRELIMINARY;
Q93VKS;
   PRINTS; PR00463; EP450I.
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PRINTS; PR00463; EP4501
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                                                                                                                                                                                                                                          Local Similarity
Les 8; Conserv
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                                                                                                                             fransmembrane
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Matches
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Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D., Maiti R., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R.,
Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
-! SIMILARITY: Belongs to the cytochrome P450 family.
EMBL, AC079041; A8450718.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MUCLEOTIDE SEQUENCE.
MEDLINE-21555285; PubMed=11759840;
MEDLINE-21555285; PubMed=11759840;
Manachar T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
Matanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
Yasuda M., Tabata S.,
"Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
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Pred. No. 10;
0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc
NCBI_TaxID=103690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   350 AA; 39119 MW; 0AB1C62658675201 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
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GO; GO:0004497; F:monoxygenase activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR001128; Cytochrome_P450.
InterPro; IPR002401; EP4501.
                                                                                                                                                                                                              350 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AP003605; BAB77491.1; -; Genomic_DNA.
PIR; AR2572; AF2572.
                                                                                                                                                                                                                                                                         Created)
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                                  :: |:|: | | | : | | | | 113 VIERISDIFAGLGFQVAEGP 132
   20
                                                                                                                                                                                                                                                                                                                                                           Alr9005 protein.
OrderedLocushames=alr9005;
Anabaena sp. (strain PCC 7120).
Plasmid pCC7120epsilon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              313 VDEALKAKGFVIAENPLW 330
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1 LVAEVSEFLFGSGFAIAEGP
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01-JUN-2001 (TrEMBLrel. 17,
01-MRR-2004 (TrEMBLrel. 26,
Cytochrome P450, putative.
                                                                                                                                                                                                     QBYJV8 ANASP PRELIMINARY;
QBYJV8;
01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                               01-MAR-2002 (TrEMBLrel. 20, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA Res. 8:205-213(2001).
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Q9C6SO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 61.1 tes 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002401; El
Pfam; PF00067; p450; 1.
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08 2708
AND 10 08 470
AC 08 270
DT 01-MA
DT 01-MA
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DB ANADA
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090650 ARA
10 090658
AC 090658
AC 091-JU
DT 01-JU
DE CATE
OC FREAZ
OC FREA
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Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
Ishida J., Jiang P.X., Jones T., Kamiya A., Karliin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
Nguyen M., Omodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
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Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka
Mguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai
Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons, rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kim C.J., Chen H., Cheuk R., Shinn P., Bowser L., Carninci P., Chan M.M., Chang C.H., Dale J.M., Deng J.M., Hayashizaki Y., Hauan V.W., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Le J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Wallender E.K., Wong C., Wu Yamada K., Yu G., Yuan S., Davis R.W., Theologis A., Ecker J.R.; Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the cytochrome P450 family.
                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                            2; Length 593;
PRINTS; PR00385; P450.
PROSITE; P800086; CYTOCHROME P450; UNKNOWN 1.
Heme; Iron, Metal-binding; Monooxygenase; Öxidoreductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
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Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                        593 AA; 66643 MW; E80CBE9B8B2BD199 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
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GO; GO:0004497; F:monoxygenase activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR001128; Cytcohrome_P450.
InterPro; IPR002401; EP4501.
                                                                                                                                                                                                                                                                  ilarity 36.4%; Score 54; DB 36.4%; Pred. No. 24; Conservative 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   At1g31800/68069 m00159.
Arabidopsis thaTiana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AY056446; AAL08302.1; -; mRNA.
EMBL; AY142017; AAM98281.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          174 ILAEILDFVMGKGLIPADGEIW 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LVAEVSEFLFGSGFAIAEGPLW 22
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Rickettsiaceae; Rickettsieae; Rickettsia; spotted fever group
                                                                                                                                   Science 293:2093-2098(2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=lpxK;
Rickettsia rickettsii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
               NCBI_TaxID=781;
                                                                                                                                                                                                                                                                    phosphate)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LPXK RICRI
P58187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032."; submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
PubMed=12948626; DOI=10.1016/S0168-1656(03)00154-8;
Ralinowski J., Bathe B., Bartels D., Bischoff N., Bott M.,
Burkovski A., Dusch N., Eggeling L., Eikmanns B.J., Gaigalat L.,
Goesmann A., Huthmacher K., Kraemer R., Linke B.,
MCHardy A.C., Meyer P., Moeckel B., Pfefferle W., Puehler A.,
Rey D.A., Rueckert C., Rupp O., Sahm H., Wendisch V.F., Wiegraebe I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The complete Corynebacterium glutamicum ATCC 13032 genome sequence and its impact on the production of L-aspartate-derived amino acids and vitamins.";
J. Biotechnol. 104:5-25(2003).

EMBL: BA000036; BAB98745.1; -; Genomic_DNA.

EMBL: BX927152; CAF21362.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-FEB-2003 (Rel. 41, Created)
8-FEB-2003 (Rel. 41, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Tetraacyldigaccharide 4'-kinase (EC 2.7.1.130) (Lipid A 4'-kinase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3;
                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
                                                                                                                                                                                                                             QBNQS2 CORGL PRELIMINARY; PRT; 97 AA.

QBNQS2, Q6M5K5;

QBNQS2, Q6M5K5;

01-OCT-2002 (TrEMBLrel. 22, Created)

13-SEP-2005 (TrEMBLrel. 31, Last annotation update)

Hypothetical membrane protein (Putative membrane protein).

OrderediocusNames=c911352, c91524;

Corynebacterium glutamicum (Brevibacterium flavum).

Bacteria, Actinobacteria, Actinobacteridae;

Corynebacterineae; Corynebacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 52.5; DB 2; Length 97; Pred. No. 7.3;
                                                                               44.3%; Score 54; DB 2; Length 595; 36.4%; Pred. No. 24;
                PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN 1.
Heme; Iron; Metal-binding; Monooxygenase; Oxidoreductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Indels
                                                                                                          7; Indels
                                                       595 AA; 66846 MW; A548A33A48323B7D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteome; Hypothetical protein.
SEQUENCE 97 AA; 10570 MW; 14FAB3646A259D46 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  321 AA
                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                         7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LVAEVSEFL---FGSGFAIAEGPLWT 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLAMVSTALRIRFGSGVALAATVLWT 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=1pxK; OrderedLocusNames=RC1092; Rickettsia conorii.
                                                                                                                                                    176 ILAEILDFVMGKGLIPADGEIW 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                     1 LVAEVSEFLFGSGFAIAEGPLW 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch
1 Similarity 57.7%;
15; Conservative 1
                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
     PRINTS; PR00385; P450.
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NUCLEOTIDE SEQUENCE.
                                                                                           Similarity
8; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1718;
                                             Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                         Nakagawa S.;
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                                                                                Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rauch A.;
                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               092GN1;
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                                                                                                                                                                                                      RESULT 13
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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"Pseudogenes, junk DNA, and the dynamics of Rickettsia genomes.";
Mol. Biol. Evol. 18:829-839(2001).
-!- FUNCTION: Transfers the gamma-phosphate of ATP to the 4'-position of a tetraacyldisaccharide 1-phosphate intermediate (termed DS-1-p) to form tetraacyldisaccharide 1,4'-bis-phosphate (lipid IVA)
                                                                                                                                                                                                                                                                                                   -i- FUNCTION: Transfers the gamma-phosphate of ATP to the 4'-position of a tetraacyldisaccharide 1-phosphate intermediate (termed DS-1-P) to form tetraacyldisaccharide 1,4'-bis-phosphate (lipid IVA)
                                                                                                                                                                                                                                                                                                                                                                                                                                (By similarity).

CATALYTIC ACTIVITY: AFP + (2-N,3-O-bis(3-hydroxytetradecanoyl) - beta-D-glucosaminyl) - (1->6) - (2-N,3-O-bis(3-hydroxytetradecanoyl) - beta-D-glucosaminyl phosphare) = ADP + (2-N,3-O-bis(3-hydroxytetradecanoyl) - 4-O-phosphono-beta-D-glucosaminyl) - (1->6) - hydroxytetradecanoyl) - 4-O-phosphono-beta-D-glucosaminyl) - (1->6) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                              "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
                                                                                                             Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V., Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Tetraacyldisaccharide 4'-kinase (EC 2.7.1.130) (Lipid A 4'-kinase)
                                            STRAIN=Malish 7;
MEDLINE=21442074; PubMed=11557893; DOI=10.1126/science.1061471;
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Rickettsiaceae; Rickettsieae; Rickettsia; spotted fever group.
NCBI_TaxID=783;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATP-binding, Complete proceome, Kinase, Lipid A biosynthesis, Lipid synthesis, Nucleotide-binding; Transferase.

NP BIND 54 61 ATP (Potential).

SEGURNCE 321 AA, 36059 MW, 9FF4672CE1CF99E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (2-N,3-O-bis(3-hydroxytetradecanoyl)-beta-D-glucosaminyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42.6%; Score 52; DB 1;
52.4%; Pred. No. 27;
tive 4; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- PATHWAY: Lipid A blosynthesis; sixth step.
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     321 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE008660; AAL03630.1; -; Genomic_DNA.

PIR; D97836; D97836.

HAMAP; MF 00409; -; 1.

Interpro; IDXK; 1.

Pfam; PF02666; LpXK.

TIGRFAMB; TIGR00682; lpXX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               155 IVSVDSQRLFGNGFLIPAGPL 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LVAEVSEFLFGSGFAIAEGPL 21
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16-OCT-2001 (Rel. 40, Last seq
13-SEP-2005 (Rel. 48, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE 321 AA; 36059 MW;
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics, and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
(By similarity).

CATALYTIC ACTIVITY: ATP + (2-N,3-0-bis(3-hydroxytetradecanoyl) - beta-D-glucosaminyl) - (1->6) - (2-N,3-0-bis(3-hydroxytetradecanoyl) - beta-D-glucosaminyl phosphate) = ADP + (2-N,3-0-bis(3-hydroxytetradecanoyl) - hydroxytetradecanoyl) - 4-0-phosphono-beta-D-glucosaminyl) - (1->6) - (2-N,3-0-bis(3-hydroxytetradecanoyl) - beta-D-glucosaminyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                    HAWAP; MF 00409; -; 1.
InterPro; IPR003758; LpxK.
Pfam; PP02606; LpxK; 1.
TIGRFAMS; TIGR00682; lpxK; 1.
ATP-binding; Kinase; Lipid A biosynthesis; Lipid synthesis; Nucleotide-binding; Transferase.
Nucleotide-binding; Transferase.
NP_BIND 54 61 APP (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
42.6%; Score 52; DB 1; Length 321;
Best Local Similarity 52.4%; Pred. No. 27;
Matches 11; Conservative 4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54 61 ATP (Potential).
321 AA; 36083 MW; 45E6CEB6CC50COAE CRC64;
                                                                                                                                  phosphate).
PATHWAY: Lipid A biosynthesis; sixth step. SIMILARITY: Belongs to the lpxK family.
                                                                                                                                                                                                                                                                                                                                                               EMBL; AJ293329; CAC33716.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 LVAEVSEFLEGSGFAIAEGPL 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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Search completed: March 7, 2006, 21:58:09 Job time: 122.8 secs

:|: |: ||:|| | ||| 155 IVSVDSQRLFGNGFLIPAGPL 175

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model Run on:

March

7, 2006, 21:43:03; Search time 234.8 Seconds . (without alignments) 44.911 Million cell updates/sec

US-10-751-235-10 Perfect score: ritle:

1 LVAEVSEFLFGSGFAIAEGPLWTA 24 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

2443163 seqs, 439378781 residues Searched:

2443163 . Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s:\* Genesed Database

geneseqp2003as:\* geneseqp2003bs:\* geneseqp1990s:\* geneseqp2000s:\* geneseqp2002s:\* geneseqp2001s:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:\* geneseqp2005s:\*

	Description	Aeb16912 Cytochrom	Aeb16908 Thale cre	Adt56240 Plant pol		-	Ady22850 Plant ful	Aeb16919 Barley cy	Aeb16918 Rice cyto	Aeb16954 Rice cyto	Abu25025 Protein e	Abu25075 Protein e	Aeb16936 Rice cyto	Adx67984 Plant ful	Aeb16939 Wheat cyt	Aeb16937 Barley cy	Abb54899 Lactococc	Ads28360 Bacterial	Aeb16940 Tomato cy	Aeb16935 Thale cre	Aag91239 C glutami	Ä	Abu33039 Protein e	Ads28192 Bacterial	Adn25200 Bacterial
SUMMARIES	ID	AEB16912	AEB16908	ADT56240	AEB16923	AEB16920	ADY22850	AEB16919	AEB16918	AEB16954	ABU25025	ABU25075	AEB16936	ADX67984	AEB16939	AEB16937	ABB54899	ADS28360	AEB16940	AEB16935	AAG91239	ABB49267	ABU33039	ADS28192	ADN25200
	DB	6	σ	œ	O	σ	8	σ	0	σ	9	9	σ	œ	σ	σ	Ŋ	ω	0	σ	4	'n	9	æ	80
	Query Match Length	24	539	260	208	362	382	545	561	588	167	342	632	662	342	208	324	344	579	595	97	350	350	287	360
de	Query	100.0	100.0	100.0	93.4	90.5	90.2	90.5	90.2	90.2	48.4	48.4	47.5	47.5	46.7	46.7	45.9	45.9	44.3	44.3	43.0	41.0	41.0	40.6	40.2
	Score	122	122	122	114	110	110	110	110	110	59	59	28	58	57	57	99	26	54	54	52.5	20	20	49.5	49
	Result No.	н	7	٣	4	ß	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24

Drosophil	Drosophil	Drosophil	dIndyaa s	Drosophil	Protein e	Bacterial	M. xanthu	Plant ful	Plant hom	Baeyer-Vi	Oil-assoc	Bacterial	Human can	Novel mar	Plant ful	Bacterial	Bacterial	Plant ful	Human dia	Pseudomon
Abb60315	Abb66903	Abb79611	Abr40099	Adp64789	Abu20163	Ads21348	Abm91222	Adx76358	Adt 87787	Adc61143	Adj49445	Adn20724	Aab43990	Aau29352	Adx88517	Ads42528	Ad822754	Adx80107	Abm84611	Abo79928
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ABB60315	ABB66903	ABB79611	ABR40099	ADP64789	ABU20163	ADS21348	ABM91222	ADX76358	ADT87787	ADC61143	ADJ49445	ADN20724	AAB43990	AAU29352	ADX88517	ADS42528	ADS22754	ADX80107	ABM84611	ABO79928
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572	572	572	572	572	173	303	316	394	483	523	1032	1124	103	168	255	326	359	489	512	683
40.2	40.2	40.2	40.2	40.2	39.3	39.3	39.3	39.3	39.3	39.3	39.3	39.3	38.9	38.5	38.5	38.5	38.5	38.5	38.5	38.5
49	49	49	49	49	48	48	48	48	48	48	48	48	47.5	47	47	47	47	47	47	47
25	56	27	28	59	30	31	32	33	. 34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1 **AEB16912** 

AEB16912 standard; peptide; 24 AA.

AEB16912;

08-SEP-2005 (first entry)

Cytochrome P450 monooxygenase transmembrane domain peptide SEQ ID NO: 10. 

Pigment, metabolic engineering, antioxidant, transgenic plant, cytochrome P450.

Unidentified.

US2005150002-A1

07-JUL-2005.

02-JAN-2004; 2004US-00751235.

02-JAN-2004; 2004US-00751235.

(DELL/) DELLAPENNA D.

(TIAN/) TIAN L. (KIMJ/) KIM J.

Kim J;

Tian L,

Dellapenna D,

WPI; 2005-487984/49.

New expression vector comprising a nucleic acid sequence encoding a polypeptide having monooxygenase P450 activity, useful in altering the carotenoid production in a plant for enhancing production of specific carotenoid compounds.

Claim 6; SEQ ID NO 10; 135pp; English.

The present invention relates to genes, proteins and methods comprising carotenoid monooxygenases in the cytochrome P450 family. The invention also relates to altering carotenoid ratios in plants and microorganisms using LUT1 epsilon-hydroxylases and/or CYP97h beta-hydroxylases. The invention is useful in altering the carotenoid production in a plant for enhancing production of specific carotenoid compounds that are potent antioxidants. The present sequence is a cytochrome P450 monooxygenase conserved transmembrane domain peptide.

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Kovalic DK;
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Matches
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ADT56240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pigment; metabolic engineering; antioxidant; transgenic plant; CYP97Cl; cytochrome P450 97Cl.
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                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Encoded by bases of positions 942 to 1037"; 332. .333. .352. .352. .352. .352. .352. .352. /note= "Encoded by bases of positions 1242 to 1326' 347. .352. .366 /note= "Encoded by bases of positions 1420 to 1523" 413. .414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Encoded by bases of positions 2340 to 2440"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Encoded by bases of positions 496 to 650" 265. .266
                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                  Thale cress LUT1 (cytochrome P450 97C1) protein, SEQ ID NO: 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anotes "Encoded by bases of positions 1662 149. 450 (notes "Encoded by bases of positions 1839
                                            Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             476. .477
/note= "Encoded by bases of positions 2081
                     note= "Cysteine motif region"
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                                                                                                                                     1 LVAEVSEFLFGSGFAIAEGPLWTA 24
                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                              AEB16908 standard; protein; 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-JAN-2004; 2004US-00751235.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-JAN-2004; 2004US-00751235.
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                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                         24; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (DELL/) DELLAPENNA (TIAN/) TIAN L.
                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference
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  Sequence 24 AA;
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(KIMJ/) KIM J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dellapenna D,
                                                                                                                                                                                                                                                                                                                                                                                       08-SEP-2005
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                                                                                                                                                                                                                                                                                                                                             AEB16908;
                                            Query Match
Best Local
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Matches
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AEB16908
AXX
AEB16908
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AEB16908
AXX
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AEB16908
AXX
AXX
AEB16908
AEB169
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The invention relates a recombinant DNA construct comprising a polynucleotide having any of 5544 nucleotide sequences (CDNAS SEQ ID NO: 15544) and encoding a polypeptide with any of 5544 amino acid sequences (SEQ ID NO: 5545-11088). The CDNAs and proteins are from corn, soybean, Arabidopsis, wheat and rape but the specification does not indicate which sequences is derived from which organism. Also included is a method of producing a plant having an improved property, comprising transforming a plant with a recombinant DNA construct comprising a promoter region functional in a plant cell operably joined to a polynucleotide encoding a polypeptide associated with the property, and growing the transformed plant. The property is selected from improving plant cold tolerance, for manipulating growth rate in plant cells by modification of the cell cycle
                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New recombinant DNA constructs useful in the field of biochemistry and genetics, and in particular for producing transgenic plants with improved biological characteristics.
The present invention relates to genes, proteins and methods comprising carotenoid monooxygenases in the cytochrome P450 family. The invention also relates to altering carotenoid ratios in plants and microorganisms using LUT1 epsilon-hydroxylases and/or CYP97A beta-hydroxylases. The invention is useful in altering the carotenoid production in a plant for enhancing production of specific carotenoid compounds that are potent antioxidants. The present sequence is thale cress LUT1 [cytochrome P450 monooxygenase (CYP97C1); At3953130 gene] protein. Note: The current sequence is that of thale cress LUT1 protein that is encoded by cDNA located on chromosome 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plant; transgenic; cold tolerance; growth rate; drought tolerance; disease resistance; galactomannan production; plant growth regulator; heat tolerance; herbicide tolerance; lignin production; extreme osmotic condition tolerance; pathogens resistance; pest resistance; yield improvement; seed oil yield; seed protein yield.
                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                              Length 539;
                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                           100.0%; Score 122; DB 9;
100.0%; Pred. No. 5.4e-11;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; SEQ ID NO 6317; 14pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADT56240 standard; protein; 560 AA
                                                                                                                                                                                                                                                                                                                                                                                                          1 LVAEVSEFLFGSGFAIAEGPLWTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plant polypeptide, SEQ ID 6317.
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28-APR-2003; 2003US-00425115.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-JAN-2005 (first entry)
                                                                                                                                                                                                                                                                                                                                 Local Similarity 100.
1es 24; Conservative
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                                                                                                                                                                                                                                                                     Sequence 539 AA;
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pathway, for improving plant drought tolerance, for providing increased resistance to plant disease, for galactomannan production, for production of plant growth regulators, for improving plant heat tolerance, for improving plant tolerance to herbicides, for increasing the rate of homologous recombination in plants, for lignin production, for improving plant tolerance to extreme osmotic conditions, for improving plant tolerance to extreme osmotic conditions, for improving plant tolerance to pathogens or pests, for yield improvement by modification of carbohydrate, nitrogen or phosphorus use and/or uptake and for yield improvement by providing improved plant growth and can gevelopment under at least one stress condition. The polymuclectide may development under at least one stress condition. The polymuclectide may calso encode a plant transcription factor. The methods and compositions of the present invention are useful in the field of biochemistry and capentics in particular for producing transgenic plants with improved bloogical characteristics such as increased yield, improved nitrogen of tolerance to extreme osmotic and drought conditions, and improved nitrogen flow, increasing plant tolerance to cold or heat, improved nitrogen of the present extreme osmotic and drought conditions, and improving plant colerance to plant pests or pathogens. They can also be used in physical arrays of molecules, plant breeding markers, computer-based storage and analysis systems. The present sequence is one of the 5544 plant protein carrays of molecules, plant breeding markers, computer-based storage and analysis systems. The present sequence is one of the 5544 plant protein cefectronic format directly from USPTO at

celectronic format directly from USPTO at

celectronic format directly from USPTO at

celectronic format directly from USPTO at
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100.0%; Score 122; DB 8; Length 560; 100.0%; Pred. No. 5.6e-11; tive 0; Mismatches 0; Indels
                              0; Mismatches
                                                                           165 LVAEVSEFLFGSGFAIAEGPLWTA 188
                                                         1 LVAEVSEFLFGSGFAIAEGPLWTA 24
               Local Similarity 100.
   Query Match
                               Matches
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AEB16923 standard; protein; 208 AA. AEB16923; AEBIGESTA 4
AEBIGESS AEBIGESS AEBIGESS AEBIGESS AEBIGESS ACCAEBIGES ACCAEBIGE

(first entry) 08-SEP-2005 Sunflower cytochrome P450 97C (CYP97C) protein, SEQ ID NO: 21.

Pigment; metabolic engineering; antioxidant; transgenic plant; CYP97C; cytochrome P450 97C.

Helianthus annuus.

US2005150002-A1

07-JUL-2005.

02-JAN-2004; 2004US-00751235

02-JAN-2004; 2004US-00751235.

DELL/) DELLAPENNA D.

(TIAN/) TIAN L. (KIMJ/) KIM J.

Kim J;

Dellapenna D, Tian L,

WPI; 2005-487984/49.

N-PSDB; AEB16929

3ENBANK; BQ971938.

New expression vector comprising a nucleic acid sequence encoding a polypeptide having monooxygenase P450 activity, useful in altering the carotenoid production in a plant for enhancing production of specific

carotenoid compounds. 

Claim 9; SEQ ID NO 21; 135pp; English.

The present invention relates to genes, proteins and methods comprising carotenoid monooxygenases in the cytochrome P450 family. The invention also relates to altering carotenoid ratios in plants and microorganisms using LUT1 epsilon-hydroxylases and/or CYP97A beta-hydroxylases. The invention is useful in altering the carotenoid production in a plant for enhancing production of specific carotenoid compounds that are potent antioxidants. The present sequence is sunflower cytochrome P450 monooxygenase (CYP97C) protein.

Sequence 208 AA;

ö Score 114; DB 9; Length 208; Pred. No. 3.6e-10; 0; Mismatches 1; Indels ö ch 93.4%; 1 Similarity 95.8%; 23; Conservative Query Match Best Local Similarity Matches 23; Conserv

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Gaps

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RESULT 5 AEB16920

AEB16920 standard; protein; 362

AEB16920;

08-SEP-2005 (first entry)

Wheat cytochrome P450 97C (CYP97C) protein, SEQ ID NO: 18.

Pigment; metabolic engineering; antioxidant; transgeníc plant; CYP97C; cytochrome P450 97C.

Triticum aestivum.

US2005150002-A1.

07-JUL-2005

02-JAN-2004; 2004US-00751235

02-JAN-2004; 2004US-00751235

DELLAPENNA D. TIAN L. (DELL/) DELLAPEN (TIAN/) TIAN L. (KIMJ/) KIM J.

Dellapenna D,

WPI; 2005-487984/49.

N-PSDB; AEB16926. GENBANK; CA497665, BG906289, CA742365, CA742792.

New expression vector comprising a nucleic acid sequence encoding a polypeptide having monooxygenase P450 activity, useful in altering the carotenoid production in a plant for enhancing production of specific carotenoid compounds. 

Claim 9; SEQ ID NO 18; 135pp; English.

The present invention relates to genes, proteins and methods comprising carotenoid monooxygenases in the cytochrome P450 family. The invention also relates to altering carotenoid ratios in plants and microorganisms using iuTi: epsilon-hydroxylases and/or CYP97A beta-hydroxylases. The invention is useful in altering the carotenoid production in a plant for enhancing production of specific carotenoid compounds that are potent antioxidants. The present sequence is wheat cytochrome P450 monooxygenase (CYP97C) protein.

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07-JUL-2005
                                    invention.
                                                                                                                                                              109
                                                                                                                                                                                                                                                    AEB16919;
                                                                                                                                                                                                  RESULT 7
                                                                                                                                                                                                               AEB16919
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8833333
                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention describes a recombinant DNA construct comprising a polymucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent Offlice available in electronic form from the US patent Offlice available in electronic form from the US patent Offlice as a mino acid sequence. The second of the construct is useful for the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, for manipulating growth rate in semicic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, lightin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one
                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for conferring increased resistance to plant disease, or for
                                                                                                                                                                                                                                                             plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance; extreme osmotific condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield;
                                                 Gaps
                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cao Y;
                      Length 362;
                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tabaska JE,
                                                                                                                                                                                                                                       Plant full length insert polypeptide segid 70634.
                      90.2%; Score 110; DB 9; 95.7%; Pred. No. 3.2e-09;
                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Screen SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 70634; 15pp; English.
                                                                                       1 LVAEVSEFLFGSGFAIAEGPLWT 23
                                                                                                                                                               ADY22850 standard; protein; 382 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-APR-2003; 2003US-00425114.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kovalic DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-00304517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-NOV-2001; 2001US-00985678
                                                                                                                                                                                                               (first entry)
                                                 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZHOU Y.
KOVALIC D K.
SCREEN S E.
TABASKA J E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-180133/17.
                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhou Y,
Sequence 362 AA;
                                                                                                                                                                                                                                                                                                                                                                                                      US2004034888-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              improving yield
                                                                                                                                                                                                                                                                                                                                                      protein content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZHOU Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIU J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAO Y.
                                                                                                                                                                                                                                                                                                                                                                            Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-MAY-1999;
                                                                                                                                                                                                               21-APR-2005
                                                                                                                                                                                                                                                                                                                                                                                                                               19-FEB-2004.
                                                                                                                                                                                        ADY22850;
                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (LIUJ/)
(ZHOU/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (KOVA/)
(SCRE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TABA/)
(CAOY/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liu J,
                                                 Matches
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stress condition or for modifying seed oil or protein yield and/or content. This is the amino acid sequence of a plant full length insert polypeptide that can be used in the recombinant DNA construct of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pigment; metabolic engineering; antioxidant; transgenic plant; CYP97C; cytochrome P450 97C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New expression vector comprising a nucleic acid sequence encoding a polypeptide having monooxygenase P450 activity, useful in altering the carchenoid production in a plant for enhancing production of specific caroteenoid compounds.
                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Barley cytochrome P450 97C (CYP97C) protein, SEQ ID NO: 17.
                                                                                                                                                                                                                               Length 382
                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                         Score 110; DB 8;
Pred. No. 3.4e-09;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Encoded by AGN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 9; SEQ ID NO 17; 135pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                              LVABVSEFLFGSGFAIAEGDLWT 131
                                                                                                                                                                                                                                                                                                                                                           23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AEB16919 standard; protein; 545 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hordeum vulgare; subsp. vulgare.
Hordeum vulgare; subsp. spontaneum.
                                                                                                                                                                                                                                                                                                                                                       1 LVAEVSEFLFGSGFAIAEGPLWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kim J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-JAN-2004; 2004US-00751235.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-JAN-2004; 2004US-00751235
                                                                                                                                                                                                                            Query Match
Best Local Similarity 95.7%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-SEP-2005 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dellapenna D, Tian L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (DELL/) DELLAPENNA D.
(TIAN/) TIAN L.
(KIMJ/) KIM J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2005-487984/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AEB16925
                                                                                                                                                                     Sequence 382 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 545 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US2005150002-A1
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AEB16918;

RESULT 8

AEB1691

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The present invention relates to genes, proteins and methods comprising carotenoid monooxygenases in the cytochrome P450 family. The invention also relates to alternoid carotenoid ratios in plants and microorganisms using LUT1 epsilon-hydroxylases and/or CYP97A beta-hydroxylases. The invention is useful in altering the carotenoid production in a plant for emhancing production of specific carotenoid compounds that are potent antioxidants. The present sequence is rice cytochrome P450 monooxygenase (CYP97B4) protein.
                                                                                                               Pigment; metabolic engineering; antioxidant; transgenic plant; CYP97B4; cytochrome P450 97B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antisense, prokaryotic essential gene, cell proliferation, drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New expression vector comprising a nucleic acid sequence encoding a polypeptide having monooxygenase P450 activity, useful in altering the carotenoid production in a plant for enhancing production of specific carotenoid compounds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90.2%; Score 110; DB 9; Length 588; 95.7%; Pred. No. 5.6e-09; ive 0; Mismatches 1; Indels
                                                                                Rice cytochrome P450 97B4 (CYP97B4) protein, SEQ ID NO: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein encoded by Prokaryotic essential gene #10552.
                                                                                                                                                                                Oryza sativa; japonica cultivar-group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 9; SEQ ID NO 52; 135pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 LVAEVSEFLFGSGFAIAEGPLWT 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABU25025 standard; protein; 167 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kim J;
                                                                                                                                                                                                                                                                                                    02-JAN-2004; 2004US-00751235
                                                                                                                                                                                                                                                                                                                                           02-JAN-2004; 2004US-00751235
                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tian L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clostridium difficile.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2005-487984/49.
                                                                                                                                                                                                                                                                                                                                                                                  DELLAPENNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 588 AA;
                                                                                                                                                                                                                       US2005150002-A1
                                                                                                                                                                                                                                                                                                                                                                                                   (TIAN/) TIAN L.
(KIMJ/) KIM J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200277183-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dellapenna D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; E017117.
                                           08-SEP-2005
                                                                                                                                                                                                                                                            07-JUL-2005
      AEB16954;
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                                                                                                                                                                                                                                                                                                                                                                                  (DELL/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to genes, proteins and methods comprising carotemoid monooxygenases in the cytochrome P450 family. The invention also relates to altering carotemoid ratios in plants and microorganisms using LUT1 epsilon-hydroxylases and/or CYP97A beta-hydroxylases. The invention is useful in altering the carotemoid production in a plant for antioxidants. The present sequence is rice cytochrome P450 monooxygenase (CYP97C1) protein.
                                                                                                                                                                                                                                                                                                                                                                                Pigment, metabolic engineering, antioxidant, transgenic plant, CYP97C2, cytochrome P450 97C2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New expression vector comprising a nucleic acid sequence encoding a polypeptide having monooxygenase P450 activity, useful in altering the carotenoid production in a plant for enhancing production of specific
                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                           ö
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Score 110; DB 9; Length 545;
Pred. No. 5.1e-09;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 90.2%; Score 110; DB 9; Length 561; Local Similarity 95.7%; Pred. No. 5.3e-09; nes 22; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                       Rice cytochrome P450 97C2 (CYP97C2) protein, SEQ ID NO: 16.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa; japonica cultivar-group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 9; SEQ ID NO 16; 135pp; English.
                                                                                                       LVAEVSEFLFGSGFAIAEGALWT 174
                                                                                23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 LVAEVSEFLFGSGFAIAEGPLWT 23
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                                                                              1 LVAEVSEFLFGSGFAIAEGPLWT
                                                                                                                                                                                                                   AEB16918 standard; protein; 561
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  90.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-JAN-2004; 2004US-00751235.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-JAN-2004; 2004US-00751235
                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dellapenna D, Tian L,
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(TIAN/) TIAN L.
(KIMJ/) KIM J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2005-487984/49.
N-PSDB; AEB16924.
GENBANK; AAK20054.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          carotenoid compounds
                                                                                                                                                                                                                                                                                                  (first
                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 561 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JS2005150002-A1
                                                                                                                                                                                                                                                                                                    08-SEP-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-JUL-2005.
                                         22;
Query Match
Best Local S
Matches 22
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Gaps

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03-OCT-2002

AEB16954 standard; protein; 588 AA.

AEB16954 ID AEB.

RESULT 9

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Query Match

Best Loc Matches

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New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                      Antisense; prokaryotic essential gene; cell proliferation; drug design.
Protein encoded by Prokaryotic essential gene #10602
                                                                                                                                                                                                                                                                                                                                                               claim 25; SEQ ID NO 52999; 1766pp; English.
                                                                                                                      21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                            06-MAR-2002; 2002US-0362699P
                                                                                                                                                                                                                   (ELIT-) ELITRA PHARM INC
                                               Clostridium difficile.
                                                                                                                                                                                                                                                                             WPI; 2003-029926/02.
                                                                                                                                                                                                                                                                                         N-PSDB; ACA28945
                                                                      WO200277183-A2.
                                                                                                                                            21-MAR-2001;
                                                                                                                                                         06-SEP-2001;
                                                                                                                                                                   25-OCT-2001;
08-FEB-2002;
                                                                                              03-OCT-2002
                                                                                                                                                                                                                                           Wang
 New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                     Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                    any one
                                                                                                                                                                                                                                                                 invention relates to an isolated nucleic acid comprising
                                                                                                                      Ohlsen KL,
Forsyth RA,
                                                                                                                      Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48.4%; Score 59; DB 50.0%; Pred. No. 0.3; ive 5; Mismatches
                                                                                                                                                                                                                                           Claim 25; SEQ ID NO 52949; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences
                                                                                                                      Malone C,
Carr GJ,
                                   2001US-00948993.
2001US-0342923P.
2002US-00072851.
21-MAR-2002; 2002WO-US009107
                         2001US-00815242
                                                                       06-MAR-2002; 2002US-0362699P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 50.0
Matches 10; Conservative
                                                                                               (ELIT-) ELITRA PHARM INC.
                                                                                                                     Zamudio C,
Trawick JD,
                                                                                                                                                         WPI; 2003-029926/02.
                                                                                                                                                                       N-PSDB; ACA28895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 167 AA;
                                              25-OCT-2001;
08-FEB-2002;
                       21-MAR-2001;
                                                                                                                      Wang L,
Wall D,
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invention relates to an isolated nucleic acid comprising any one

Zyskind JW; Xu HH;

Ohlsen KL, · Forsyth RA,

Haselbeck R, Yamamoto R,

Malone C, Carr GJ,

Zamudio C, Trawick JD,

'n'n

2001US-00948993. 2001US-0342923P. 2002US-00072851.

2001US-00815242

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The fill antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound sectivity, (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains in solutions or collection of strains in specification of an organism. The antisense mucleic acids are useful for the proliferation of an organism. The antisense mucleic acids required for cellular proliferation to isolate encledules for required correcting and an organism. The proliferation of an organism. The antisense mucleic acids required for cellular proliferation of an organism. The proliferation of an organism of the captured in the proliferation of an organism. The proliferation of an organism of the captured in a confound mucleic acids required for the proliferation of the proliferation of an organism of the proliferation of an organism of the proliferation of an organism of 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the princed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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50.0%; Pred. No. 0.7;
cive 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ftp.wipo.int/pub/published_pct_sequences
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116 IIDEVTDIFIGMGFSIAEGP 135
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ses 10; Conserv
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Gaps

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5; Indels

ABU25075 standard; protein; 342 AA

RESULT 11 ABU25075 (first entry)

19-JUN-2003 ABU25075;

8 X X X E X

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DB 6; Length 167;

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Gaps

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9

Length 632; IndelB

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Score 58; DB 9 Pred. No. 2.1; 7; Mismatches

h 47.5%; Similarity 40.9%; 9; Conservative

22

1 LVAEVSEFLFGSGFAIAEGPLW

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carotenoid monooxygenases in the cytochrome P450 family. The invention also relates to altering carotenoid ratios in plants and microorganisms using LUT1 epsilon-hydroxylases and/or CYP97A beta-hydroxylases. The invention is useful in altering the carotenoid production in a plant for enhancing production of specific carotenoid compounds that are potent antioxidants. The present sequence is rice cytochrome P450 monooxygenase (CYP97A) protein.
                                                                                                                            Query Match
Best Local Similarity
                                                                                                       Sequence 632 AA;
                                                                                                                                         Best Loc
Matches
  888888888888
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                                                                                                                                                     Pigment; metabolic engineering; antioxidant; transgenic plant; CYP97A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note= "Encoded by bases of positions 2015 to 2301" 175. .476 'note= "Encoded by bases of positions 2380 to 3051"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Encoded by bases of positions 4776 to 4856"
                                                                                                                                                                                                                                                                                                                                             /note= "Encoded by bases of positions 1229 to 1336"
                                                                                                                                                                                                                                                                                                                                                                         to 1584"
                                                                                                                                                                                                                                                                                                                                                                                                'note= "Encoded by bases of positions 1678 to 1763"
                                                                                                                                                                                                                                                                                                                                                                                                                          to 2009"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   to 2139"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to 4418"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to 4715"
                                                                                                                                                                                                                                                                                                                       to 1042"
                                                                                                                                                                                                                               33. .94
'note= "Encoded by bases of positions 277 to 379"
                                                                                                                                                                                                                                                                                              to 850"
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                                                                                                                                                                                                                                                                                                                                                                                                             409. .410
/note= "Encoded by bases of positions 1857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Encoded by bases of positions 4476 562. .563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "Encoded by bases of positions 3175
                                                                                                                                                                                                                                                                                                                                                                 note= "Encoded by bases of positions 1493
                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference 420. .421 //notes "Encoded by bases of positions 2037
                                                                                                                                                                                                                                                                                                       225. .226
note= "Encoded by bases of positions 956
889. .290
                                                                                                                                                                                                                                                                                            /note= "Encoded by bases of positions 758
                                                                                                                           Rice cytochrome P450 97A (CYP97A) protein, SEQ ID NO: 34.
                                                                                                                                                                                                                                                      164. .165
/note= "Encoded by bases of positions
188. .189
                                                                                                                                                                                          Oryza sativa; japonica cultivar-group
                                                                                                                                                                                                                   Location/Qualifiers
                                                  AEB16936 standard; protein; 632 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kim J;
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N-PSDB; AEB16944, AEB16945:
DDBJ; AP004028.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .519
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                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                            Misc-difference 343. .344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dellapenna D, Tian L,
                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference 376.
                                                                                                                                                                                                                                                                                                                                   Misc-difference 289.
                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference 409.
                                                                                                                                                                                                                                                                               Misc-difference 188.
                                                                                                                                                                                                                                                                                                          Misc-difference 225.
                                                                                                                                                                cytochrome P450 97A
                                                                                                                                                                                                                                                       Misc-difference 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference 447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference 562
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(TIAN/) TIAN L.
(KIMJ/) KIM J.
                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
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                                                                                                    08-SEP-2005
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                                                                           AEB16936;
                           RESULT 12
                                       AEB1 693
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New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for conferring increased resistance to plant disease, or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention describes a recombinant DNA construct comprising a polymucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at ftp.seqdata.uspto.gov/sequence.hml?DocID:2004034888. The polymucleotide of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for
                                                                                                                                                                                                              plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breading marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistence; galactomanan production; dispanse resistence; galactomanan production; dignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cao Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tabaska JE,
                                                                                                                                                                               Plant full length insert polypeptide seqid 38827.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Screen SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 38827; 15pp; English.
190 ILAKILKÝVMGTGLIPADGKIW 211
                                                                                 Ä
                                                                               ADX67984 standard; protein; 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhou Y, Kovalic DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-MAY-1999; 99US-00304517, 05-NOV-2001; 2001US-00985678.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-APR-2003; 2003US-00425114
                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZHOU Y.
KOVALIC D K.
SCREEN S E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TABASKA J E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pests, for confeimproving yield
                                                                                                                                                                                                                                                                                                                                                                                            JS2004034888-A1
                                                                                                                                                                                                                                                                                                                               protein content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO Y.
                                                                                                                                                                                                                                                                                                                                                             Unidentified
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                                                                                                                                               21-APR-2005
                                                                                                               ADX67984;
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(ZHOU/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (KOVA/)
(SCRE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAOY/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TABA/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liu J,
                                                 RESULT 13
                                                                 ADX67984
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Var. 17. 12.

The present invention relates to genes, proteins and methods comprising

Claim 9; SEQ ID NO 34; 135pp; English

encoding a

a nucleic acid sequence encoding a P450 activity, useful in altering the for enhancing production of specific

New expression vector comprising polypeptide having monooxygenase carotenoid production in a plant

carotenoid compounds

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improving plant tolerance to cold, heat, drought, herbicides, extreme osmocic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, recombination in plantes, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This is the amino acid sequence of a plant full length insert polypeptide that can be used in the recombinant DNA construct of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pigment; metabolic engineering; antioxidant; transgenic plant; CYP97A; cytochrome P450 97A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New expression vector comprising a nucleic acid sequence encoding a polypeptide having monooxygenase P450 activity, useful in altering the carotenoid production in a plant for enhancing production of specific carotenoid compounds.
                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wheat cytochrome P450 97A (CYP97A) protein, SEQ ID NO: 37.
                                                                                                                                                                                                                             47.5%; Score 58; DB 8; Length 662;
40.9%; Pred. No. 2.2;
iive 7; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Encoded by CAGAG"
                                                                                                                                                                                                                                                                                                             225 ILAEILEFVMGTGLIPADGEIW 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                   AEB16939 standard; protein; 342 AA.
                                                                                                                                                                                                                                                                                          1 LVAEVSEFLFGSGFAIAEGPLW 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kim J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-JAN-2004; 2004US-00751235.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENBANK; CA736787, CA736801.
                                                                                                                                                                                                                 Query Match
Query Hocal Similarity 40.30,
Best Local Similarity 40.30,
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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GENBANK; CD882035.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2005-487984/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (DELL/) DELLAPENNA (TIAN/) TIAN L. (KIMJ/) KIM J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AEB16948.
DDBJ; BJ234910.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Triticum aestivum.
                                                                                                                                                                                                   Sequence 662 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US2005150002-A1
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                                                                                                                                                                          invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                 AEB16939;
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                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                     AEB16939
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The present invention relates to genes, proteins and methods comprising carotenoid monooxygenases in the cytochrome P450 family. The invention

Claim 9; SEQ ID NO 37; 135pp; English.

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also relates to altering carotenoid ratios in plants and microorganisms using LUT1 epailon-hydroxylases and/or CYP97A beta-hydroxylases. The invention is useful in altering the carotenoid production in a plant for enhancing production of specific carotenoid compounds that are potent antioxidants. The present sequence is wheat cytochrome P450 monooxygenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to genes, proteins and methods comprising carotenoid monooxygenases in the cytochrome P450 family. The invention also relates to altering carotenoid ratios in plants and microorganisms using LUT1 epsilon-hydroxylases and/or CYP97h beta-hydroxylases. The invention is useful in altering the carotenoid production in a plant for enhancing production of specific carotenoid compounds that are potent antioxidants. The present sequence is barley cytochrome P450 monooxygenase (CYP97A) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pigment; metabolic engineering; antioxidant; transgenic plant; CYP97A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New expression vector comprising a nucleic acid sequence encoding a polypeptide having monooxygenase P450 activity, useful in altering the carotenoid production in a plant for enhancing production of specific carotenoid compounds.
                                                                                                                                                                                         Gaps
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EMBL; AJ477620, AJ477618, AJ477619, AJ832622.
                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Barley cytochrome P450 97A (CYP97A) protein, SEQ ID NO: 35
                                                                                                                                                    Length 342;
                                                                                                                                                                                         .
9
                                                                                                                                                        46.7%; Score 57; DB 9;
40.9%; Pred. No. 1.5;
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DDBJ; AV939715, AV941342, AV939552, AV939556.
GENDANK; CA004011.
                                                                                                                                                                    Pred. No. 1.5;
7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hordeum vulgare; subsp. spontaneum.
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ILAEILEFVMGTGLIPADGEVW 88
                                                                                                                                                                                                                        1 LVAEVSEPLFGSGFAIAEGPLW 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hordeum vulgare; subsp. vulgare.
                                                                                                                                                                                                                                                                                                                                             AEB16937 standard; protein; 508
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-JAN-2004; 2004US-00751235.
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                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2005-487984/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytochrome P450 97A.
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(TIAN/) TIAN L.
(KIMJ/) KIM J.
                                                                                                                                                                      Best Local Similarity
Matches 9; Conserv
                                                                                          (CYP97A) protein
                                                                                                                        Sequence 342 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 508 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-JUL-2005
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us-10-751-235-10.rag
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Gaps ; 0 Query Match

46.7%; Score 57; DB 9; Length 508;
Best Local Similarity 40.9%; Pred. No. 2.4;
Matches 9; Conservative 7; Mismatches 6; Indels

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1 LVAEVSEFLEGGFAIAEGPLW 22
::||:||:||:||
66 ILABILEFVMGTGLIPADGEVW 87

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Search completed: March 7, 2006, 21:53:06 Job time : 240.8 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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OM protein - protein search, using sw model

March Run on:

7, 2006, 21:58:31 ; Search time 26.8 Seconds (without alignments) 74.038 Million cell updates/sec

US-10-751-235-10

Perfect score:

1 LVAEVSEFLFGSGFAIAEGPLWTA 24 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

572060 segs, 82675679 residues Searched:

572060 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA:\*

(cgn2\_6/ptodata/1/iaa/5\_COMB.pep:\*

(cgn2\_6/ptodata/1/iaa/6\_COMB.pep:\*)

(cgn2\_6/ptodata/1/iaa/H\_COMB.pep:\*)

(cgn2\_6/ptodata/1/iaa/PcTUS\_COMB.pep:\*)

(cgn2\_6/ptodata/1/iaa/RE\_COMB.pep:\*)

(cgn2\_6/ptodata/1/iaa/RE\_COMB.pep:\*)

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES		
Result No.	Score	Query Match	Length	DB	ID	Description	
-	52.5	43.0	94	2	US-09-605-703B-1572	Sequence 1572, Ap	
7	49	40.2	194	~	US-09-270-767-59102		
e	49	40.2	230	~	US-09-270-767-43713		
4	48	39.3	316	~	US-09-902-540-10421		
S	47	38.5	683	~	US-09-252-991A-28674		
9	46.5	38.1	190	N	US-09-134-000C-6230		
	46	37.7	55	~	US-09-513-999C-4532		
æ	46	37.7	80	~	US-09-621-976-5244	5244,	
6	46	37.7	150	7	US-09-270-767-60566	60566,	
10	46	37.7	250	7	US-09-489-039A-10680	Sequence 10680, A	
11	45	36.9	102	7	US-09-882-434A-1	ť	
12	45	36.9	110	~	US-09-376-330-24		
13	45	36.9	131	~	US-09-513-999C-8015	80	
14	45	36.9	166	~	US-09-621-976-4638		
15	45	36.9	185	~	US-09-529-157-6		
16	45	36.9	185	N	US-09-529-157-7	7, Ap	
17	45	36.9	204	~	US-09-949-016-9489		
18	45	36.9	205	~	US-09-673-395A-205		
19	45	36.9	218	N	US-09-543-681A-4284		
20	45	36.9	329	~	US-10-152-886-51		
21	45	36.9	522	ч	US-08-305-505-2	Sequence 2, Appli	
22	. 45	36.9	561	~	US-09-489-039A-10642		
23	45	36.9	862	N	US-09-902-540-11888	Sequence 11888, A	
24	44	36.1	194	~	US-09-252-991A-31239		
25	44		519	~	US-09-248-796A-19188	191	
56	44	36.1	9	Н	US-07-803-633A-13	13,	
27	43	35.2	82	N	US-09-252-991A-23597	235	

RESULT 2 US-09-270-767-59102

Sequence 59102, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REPERBNCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 59102

LENGTH: 194

TYPE: PRT

	Sequence 14556, A	Sequence: 25022, A	Sequence 10171, A	Sequence 31301, A	Sequence 9, Appli	Sequence 7, Appli	Sequence 1, Appli	Sequence 22301, A	Sequence 4, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 1033, Ap	Sequence 6, Appli	Sequence 5, Appli	Sequence 5, Appli	Sequence 16, Appl
US-09-134-000C-3652	US-09-902-540-14556	US-09-252-991A-25022	US-09-902-540-10171	US-09-252-991A-31301	US-10-152-886-9	US-09-548-473B-7	US-09-548-473B-1	US-09-252-991A-22301	US-09-548-473B-4	US-09-858-664A-2	US-10-274-978-2	US-1.0-697-263-2	US-09-538-092-1033	US-09-548-473B-6	US-07-642-734C-5	US-08-439-009A-5	US-09-560-761B-16
~	N	~	~	~	~	~	N	~	N	~	N	7	7	~	-	~	7
188	297	310	392	411	642	871	1321	1548	1610	1665	1665	1665	1722	2596	3170	3170	404
35.2	35.2	35.2	35.2	35.2	35.2	35.2	35.2	35.2	35.2	35.2	35.2	35.2	35.2	35.2	35.2	35.2	34.8
43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	42.5
28	. 62	30	31	32	33	34	35	36	37	38	. 68	40	41	42	43	44	45

## ALIGNMENTS

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APPLICANT: Kroger: Burkhard
APPLICANT: Schooler, Hartwig
APPLICANT: Schooler, Hartwig
APPLICANT: Acider, Oskar
APPLICANT: Aberhauer, Gregor
TITLE OF INVENTION: CORTNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL
TITLE OF INVENTION: CORTNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL
TITLE OF INVENTION: CORTNEBACTERIUM GLUTAMICUM GENES ENCODING
FILE REFERENCE: BG1-129CP
CURRENT APPLICATION NUMBER: 60/142,764
PRIOR APPLICATION NUMBER: 60/142,764
PRIOR PILING DATE: 1999-09-03
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 2934
SEQ ID NO 1572
LENGTH: 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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43.0%; Score 52.5; DB 2; Length 94;
Best Local Similarity 57.7%; Pred. No. 0.41;
Matches 15; Conservative 1; Mismatches 7. τ-2-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-605-703B-1572
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ORGANISM:
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1 LVAEVSEFLFG----SGFAIAEG 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       440 LFGSFYSVAEGLEWLA 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38.5%;
56.2%;
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Best Local Similarity 56.2.
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US-09-134-000C-6230
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Sequence 1043.47.

Sequence 1043.47.

Sequence 1043.47.

Sequence 1043.47.

Sequence 1043.47.

Sequence 1043.47.

Sequence 1040.

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US-09-270-767-43713
US-09-270-767
Sequence 43713, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 43713
LENGTH: 230
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                                                                                        Score 49; DB 2; Length 194;
Pred. No. 3.7;
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                                                                                                                                                                 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 49;
Pred. No.
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US-09-252-991A-28674
; Sequence 28674, Application US/09252991A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-43713
; ORGANISM: Drosophila melanogaster US-09-270-767-59102
                                                                                                  40.2%;
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Best Local Similarity 75.0%;
Matches 9; Conservative
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Best Local Similarity 45.5
Matches 10; Conservative
                                                                 Ouery Match
Best Local Similarity 75.v.
9; Conservative
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128 FLLGGGFALAEG 139
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Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
RIOR FILING DATE: 1998-02-18
SEQ ID NOS: 33142
SEQ ID NOS: 33142
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Sequence 6230, Application US/09134000C

Rateart No. 6617156

GRNERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: NUMBER: US/09/134,000C

CURRENT APPLICATION NUMBER: US/09/134,000C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/055,778

PRIOR PRIOR FILING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812

SEQ ID NO 6230

LENGTH: 190
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Patent No. 6793961
Patent No. 6793961
Patent No. 6793961
Patent No. 6793961
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Dumas Milne Edwards, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59.US2.REG
CURRENT PAPLICATION WHORER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
CURRENT FILING DATE: 1999-02-26
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38.1%; Score 46.5; DB 2; Length 190;
Best Local Similarity 50.0%; Pred. No. 9.4;
Matches 12; Conservative 2; Mismatches 5; Indels
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Pred. No. 36;
3; Mismatches
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US-09-489-039A-10680
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US-09-882-434A-1
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; Patent No. 6703491
.; GENERAL INFORMATION:
    APPLICANT: Homburgar et al.
    TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
    FILE REFRENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; NUMBER OF SEQ ID NOS: 62517
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 46; DB.2; Length 55;
Pred. No. 2.6;
2; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTE and Encoded Human Proteins.
FILE REPERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ'ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 5244
LENGTH: 80
                                                                                                                                                                                                                                                                                           or Lys or Leu or Met
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 46; DB Pred. No. 4; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                      or Glu or Gly
                                                                                                                                                                  LOCATION: -23...1

OTHER INFORMATION: score 9.4

OTHER INFORMATION: seq SLLFICFFGESFC/IC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-621-976-5244
; Sequence 5244, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dunas Mine Edwards, J.B.
; APPLICANT: Jobert, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 50.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 37.7%;
Best Local Similarity 50.0%;
Matches 7; Conservative
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NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 4532
                                                                                                                                                                                                                                                                   LOCATION: 9
OTHER INFORMATION: Xaa= *
                                                                                                                                                                                                                                                                                                                                                           ; LOCATION: 11
; OTHER INFORMATION: Xaa= *
US-09-513-999C-4532
                                                                                                      ORGANISM: Homo sapiens
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US-09-621-976-5244
                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: UNSURE
LOCATION: 11
                                                                                                                                                                                                                                                NAME/KEY: UNSURE
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APPLICANT: GATY Breton et. al
APPLICANT: GATY Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUWONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 10680
LENGTH: 250
                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 46; DB 2; Length 250;
Pred. No. 16;
1; Mismatches 2; Indels
                                                                                                                                                                                                                       Length 150;
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                                                                                                                                                                                                                     Score 46; DB 2;
Pred. No. 8.6;
3; Mismatches
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APPLICANT: Manners, John M.
APPLICANT: Manners, John Paul
APPLICANT: Goulter, Kenneth C.
APPLICANT: Goulter, Kenneth C.
APPLICANT: Green, Jodie Lyn
ITILE GENERAL INFON: ANTI-MICROBIAL PROTEIN
FILER REFERENCE: CULLANS: LOFOLS
CURRENT APPLICATION NUMBER: US/09/882,434A
CURRENT APPLICATION NUMBER: 09/364395
PRIOR PILING DATE: 1999-07-30
PRIOR PILING DATE: 1999-07-30
PRIOR FILING DATE: 1999-11-09
PRIOR FILING DATE: 1999-11-09
PRIOR FILING DATE: 1999-10-03
PRIOR PILING DATE: 1996-11-09
PRIOR PILING DATE: 1996-01-31
NUMBER OF SEQ ID NOS: 21
SOPTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 102
                                                                                                                                             ; OTHER INFORMATION: Xaa means any amino acid US-09-270-767-60566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10680, Application US/09489039A Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/09882434A Patent No. 6909032
                                                                       TYPE: PRT
ORGANISM: Drosophila melanogaster
FEATURE:
                                                                                                                                                                                                                                                                                                                         6 SEPLFGSGFAIAEGPLWTA 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) ORGANISM: Klebsiella pneumoniae
US-09-489-039A-10680
                                                                                                                                                                                                                     Query Match
Best Local Similarity 52.6%;
Matches 10; Conservative
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 60566
LENGTH: 150
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Best Local Similarity 72.7
Matches 8; Conservative
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1 LVAEVSEFLFGSGFAIAEGPLW
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US-09-621-976-4638
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Sequence 24, Application US/09376330

Sequence 24, Application US/09376330

GENERAL INFORMATION:
APPLICANT: Tessier, Daniel C.
APPLICANT: Thomas, Daniel C.
APPLICANT: Thomas, David Y.
TITLE OF INVENTION: Method for screening for TITLE OF INVENTION: and nucleic acid encoding for UGGT

TITLE OF INVENTION: and nucleic acid encoding for UGGT

TITLE OF INVENTION: and nucleic acid encoding for UGGT

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APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Duclert, A.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT PILING DATE: 1090-02-24
PRIOR PLING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 8015
LENGTH: 131
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                                                                                                        Score 45; DB 2; Length 102;
Pred. No. 7.9;
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                                                                                      36.9%; scc...
45.0%; Pred. No. ....
... 3; Mismatches
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                                                                                                                                                                                                                                                     1 LVAEVSEFLFGSGFAIAEGP 20
                                                                                                                                                                                                                                                                                                ORGANISM: Macadamia integrifolia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:

OTHER INFORMATION: GALT-S. typ
US-09-376-330-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 FGSGFAIAEGPLWTA 24
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                                                                                                                                                Best Local Similarity 45.09
Matches 9; Conservative
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, ORGANISM: Homo sapiens
US-09-513-999C-8015
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Best Local Similarity
Matches 8; Conserve
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              ; ORGANISM: Mac
US-09-882-434A-1
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US-09-376-330-24
                                                                                                                   Query Match
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US-09-529-157-6

i Sequence 6, Application US/09529157

j Sequence 6, Application US/09529157

j Patent No. 6500939

j GENERAL INFORMATION:

j APPLICANT: Rackine, Shingo

j TITLE OF INVENTION: CDNAB Coding For Human Proteins Having Transmembrane

j TITLE OF INVENTION: Domains

j TITLE OF INVENTION: Domains

j TITLE OF INVENTION: Domains

j CURRENT APPLICATION NUMBER: US/09/529,157

j CURRENT FILING DATE: 1998-10-08

j PRIOR APPLICATION NUMBER: JP 9-276270

j PRIOR APPLICATION NUMBER: JP 9-276270

j PRIOR APPLICATION NUMBER: JP 9-276270

j PRIOR FILING DATE: 1998-10-08

j SOFTWARE: PatentIn Ver. 2.0

j SEQ ID NOS: 8

j SOFTWARE: PatentIn Ver. 2.0

j TANGER OF SEQ ID NOS: 8

j SOFTWARE: PatentIn Ver. 2.0
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36.9%; Score 45; DB 2; Length 166;
Best Local Similarity 36.4%; Pred. No. 14;
Matches 8; Conservative 5; Mismatches 9; Indels
                                                                                        RESULT 14
US-09-621-976-4638

US-09-621-976-4638

Sequence 4638, Application US/09621976

Patent No. 6639063

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Jobert, S.

TITLE OF INVENTION: ESTS and Encoded Human Proteins.

FILE REPERENCE: GENSET:054PR2

CURRENT APPLICATION UNUMER: US/09/621,976

CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335

SOFTWARE: Patent.pm

SEQ ID NO 4638

LENGTH: 166

LENGTH: 166

TYPE: PRT
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Job time : 27.8 secs
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NAME/KEY: unsure
LOCATION: (1)..(613)
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Sequence 6900, Ap
Sequence 1577, Ap
Sequence 1577, Ap
Sequence 167, App
Sequence 167, App
Sequence 121, App
Sequence 121, App
Sequence 121, App
                                                                                       March 7, 2006, 22:00:32 ; Search time 10.4 Seconds (without alignments) 46.155 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/USO8 NEW PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/USO8 NEW PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/USO7 NEW PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USO9 NEW PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/USO9 NEW PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/USIO_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/USIO_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/USIO_NEW_PUB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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-10-993-143-19
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S-10-973-115B-108
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-11-087-099-10787
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-10-873-528-167
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1-072-512-2690
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|-10-467-657-2822
|-11-087-099-6346
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                                                                                                                                                                                                                                                               135346 seqs, 20000420 residues
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1 LVAEVSEFLFGSGFAIAEGPLWTA 24
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Maximum Match 100%
Listing first 45 summaries
                                                           OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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26 41 31.6 227 6 193-10-467-657-2594 Sequence 2554, p. 27 41 31.6 227 6 193-10-467-657-2516 Sequence 2554, p. 28 41 31.6 31.2 31.2 31.4 31.6 31.2 31.2 31.4 31.6 31.2 31.2 31.4 31.6 31.2 31.2 31.0 37.0 39-516 Sequence 317.0 31.4 31.6 31.2 31.2 31.0 37.0 39-516 Sequence 317.0 31.4 31.6 31.2 31.2 31.0 37.0 39-516 Sequence 317.0 31.4 31.6 31.2 31.2 31.0 37.0 39-516 Sequence 217.0 31.4 31.6 31.2 31.2 31.0 37.0 39-516 Sequence 217.0 31.2 31.2 31.2 31.0 31.0 37.0 39-516 Sequence 217.0 31.2 31.2 31.2 31.0 31.0 31.0 37.0 39-516 Sequence 217.0 31.0 31.0 31.0 31.0 31.0 31.0 31.0 31	App			, <del>,</del> ,		
467-657-2594 Sequence 087-099-5386 Sequence 087-099-4152 Sequence 087-099-116 087-099-116 087-099-116 087-099-116 087-099-1217 087-099 087-099-1217 087-099 087-099-1217 087-099 087-099-1217 087-099-1217 087-099 087-099-1217 08	2594, 5386, 4817, 716, 72020, 7020,			зарв		•
467-657-2594 087-099-5386 087-099-5386 087-099-1152 087-099-51887 087-099-6404 467-657-1170 687-099-12171 689-642-22 112-240-28 112-3048-28 112-3048-28 112-348-28 112-348-28 112-348-28 112-348-28 112-348-28 112-348-28 112-348-28 112-348-28 112-348-28 112-348-28 112-348-28 112-348-28 112-348-28 112-348-28 112-348-28 112-348-28 112-348-28 112-348-28 112-348-28 113-3241 113-3241 12-3241 13-3241 13-3241 13-3241 13-3241 14-325 14-326 15-3241 15-3241 15-3241 15-3241 15-3241 16-328-38 16-				•-		•
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256 227 228 229 239 330 331 331 332 333 333 333 334 44 44 44 44 44 44 44 44			-099- e 121 INFO INFO AANT: JAPPE T APPE T APPE OF S. NO 12: NO NO 12: NO NO 12: NO NO 12: NO 12: NO 12: NO 12: NO 12: NO 12: NO 12: NO 12: NO 12: NO	itch al	2 4	-099- ction ANIT: ANIT: OF IN BFERE I FIL: OF SI H: 61: PRT ISM:
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APPLICANT: Kapur, Vivek and Gebhart, Connie J.
APPLICANT: Kapur, Vivek and Gebhart, Connie J.
TITLE OF INVENTION: NUCLEIC ACID AND POLYBERTIDE SEQUENCES
TITLE OF INVENTION: PROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
FILE REPERRNCE: 09531-128001
CURRENT APPLICATION NUMBER: US/11/098,686
CURRENT APPLICATION NUMBER: US/11/093/31318
PRIOR APPLICATION NUMBER: PCT/US03/31318
PRIOR PILING DATE: 2003-10-01
PRIOR PILING DATE: 2003-10-01
NUMBER OF SEQ ID NOS: 11433
SOFTWARE FARSEQ for Windows Version 4.0
SEQ ID NO 10717
LENGTH: 346
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APPLICANT: O'Toole, George

APPLICANT: O'Toole, George

APPLICANT: Trucheart, Joshua

APPLICANT: Walbridge, Michael J.

APPLICANT: Yorgey, Peter S.

APPLICANT: Yorgey, Peter S.

APPLICANT: Yorgey, Peter S.

APPLICANT: Yorgey, Peter S.

APPLICANT: NORTHON: NEUDUCTION

FILE REFERENCE: 14184-030001

CURRENT APPLICATION NUMBER: US/10/858,730

CURRENT FILING DATE: 2004-06-01

PRIOR APPLICATION NUMBER: US 60/475,000

PRIOR APPLICATION NUMBER: US 60/551,860

PRIOR APPLICATION NUMBER: US 60/551,860

PRIOR APPLICATION NUMBER: US 60/551,860

SECOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 112.
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                                                                                                             Sequence 10717, Application US/11098686
Publication No. US20060024696A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 112, Application US/10858730
Publication No. US20050255568A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Bailey, Richard B.
APPLICANT: Blomquist, Paul
APPLICANT: Doten, Reed
APPLICANT: Driggers, Edward M.
APPLICANT: Madden, Kevin T.
  229 FLTGAFGTIASGPFWT 244
                                                                                              US-11-098-686-10717
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Sequence 19, Application US/10993143

Sequence 19, Application US/10993143

Publication No. US20060036374A1

GENERAL INFORMATION:

APPLICANT: California Institute of Technology

APPLICANT: Goddard III, William A.

TITLE OF INVENTION: PRIMARY PROTEIN SEQUENCE

TITLE OF INVENTION: PRIMARY PROTEIN SEQUENCE

FILE REFERENCE: 54318-8001.US02

CURRENT APPLICATION NUMBER: US/10/993,143

CURRENT APPLICATION NUMBER: 66/218,016

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2001-07-12

NUMBER OF SEQ ID NOS: 26

SOFTWARE: Patent In version 3.3

SEQ ID NO 19

LINGTH: 246
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                                                                     Score 48.5; DB 7; Length 613; Pred. No. 7.3;
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Publication No. US20060041961A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21 (53450) B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
LENGTH: 654
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; OTHER INFORMATION: unsure at all Xaa locations
US-11-087-099-5132
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: ICCATION: (1)..(654)

: OTHER INFORMATION: unsure at all Xaa locations

US-11-087-099-10545
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Pred. No. 7.8;
6; Mismatches
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56.2%; Pred. No. 6.8;
tive 1; Mismatches
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US-10-993-143-19
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                                                                          39.8%;
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Best Local Similarity 33.3%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Triticum aestivum
                                                                                                 Best Local Similarity 33.3
Matches 10; Conservative
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Best Local Similarity
Matches 9; Conserva
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US-11-087-099-10545
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Gaps

5; Indels

Length 301;

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US-11-087-099-10787

Sequence 10787, Application US/11087099

Publication No. US20060041961A1

GENERAL INFORMATION:

APPLICANT: Abad, Mark S. et al.

TITLE OF INVENTION: Genes and Uses for Plant Improvement.

FILE REFERENCE: 38-21 (53450) B EP

CURRENT APPLICANT: APPLICANTON NUMBER: US/11/087,099

CURRENT FILING DATE: 2005-03-22

NUMBER OF SEQ ID NOS: 12464

SEQ ID NO 10787

LENGTH: 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement FILE REFERENCE: 38-21(5)450)B EP CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
LENGTH: 491
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Pred. No. 48;
5; Mismatches
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; Pred. No. 40;
· 2; Mismatches
                                                                                                                                                                                                                                        DB 24;
                                                                                                                                                                                                                                                                                 4; Mismatches
               PRIOR APPLICATION NUMBER: 10/144,156
PRIOR FILING DATE: 2002-10-05
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PastSEQ for Windows Version-4.0
SEQ ID NO 9
LENGTH: 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35.2%; Score 43; 53.3%; Pred. No.
                                                                                                                                                                                                                                        Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Pseudomonas aeruginosa PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3329, Application US/11087099
Publication No. US20060041961A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    408 LVAGTVDFIFGNGAAVLQ 425
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Best Local Similarity 44.4%;
Matches 8; Conservative
                                                                                                                                                                                                                                      Query Match
Best Local Similarity 47.1%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 EVSEFLFGSGFAIAE 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Solanum tuberosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 53.3
Matches 8; Conservative
                                                                                                                                         TYPE: PRT ORGANISM: Homo sapiens US-11-152-569-9
    CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-11-087-099-10787
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 44; DB 7; Length 505;
Pred. No. 29;
1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Indels
                                                                                                                                                                  APPLICANT: CHIRON SpA
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MAISIGNANI Vega
APPLICANT: MONACI Eligabetta
TITLE OP INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6346, Application US/11087099
Publication No. US20060041961A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
PILE REPREBRUCE: 38-21(5345)B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT PILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 6346
LENGTH: S05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Ecker, Joseph R.
APPLICANT: Nehring, Ramlah
APPLICANT: McGrath, Robert B.
TITLE OF INVENTION: ETHYLENE INSENSITIVE PLANTS
FILE REPERENCE: 532792001210
CURRENT APPLICATION NUMBER: US/11/152,569
                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
SEQ ID NO 2822
                                                                                   US-10-467-657-2822

Sequence 2822, Application US/10467657

; Publication No. US20050260581A1

; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9, Application US/11152569
Publication No. US20060005278A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151 VVELFHGMGFEVADGP 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 VSEFLFGSGFAIAEGP 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 57.1%;
Matches 8; Conservative
  149 GAAFALAAGAMWAA 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Neurospora crassa
US-11-087-099-6346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 LFGSGFAIAEGPLW 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                   FILE REPERENCE:
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US-11-087-099-6346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-467-657-2822
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Gaps

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Gaps

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Indels

Length 576;

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CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 11993
LENGTH: 461
                                                                                                                      ; TYPE: PRT
; ORGANISM: Cytophaga hutchinsonii
US-11-087-099-11993
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Sequence 5, Application US/11186731

Publication No. US20050255521A1

GENERAL INFORMATION:

APPLICANT: Kapeller-Libermann, Rosana

APPLICANT: Acton, Susan L.

TITLE OF INVENTION: Members and Uses Therefor

TITLE OF INVENTION: Members and Uses Therefor

FILE REFERENCE: MPI2001-047PIRCP1(M)

CURRENT APPLICATION NUMBER: US/11/186,731

CURRENT FILING DATE: 2005-07-21

PRIOR FILING DATE: 2005-07-21

PRIOR FILING DATE: 2001-02-15

NUMBER OF SEQ ID NOS: 9

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 5

LENGTH: 7968
                     GENERAL INFORMATION:
GURERAT APPLICATION WHERE: BANGE THEREFOR THE PRIOR APPLICATION NUMBER: US/11/186,731
CURRENT FILING DATE: 2005-02-15
FRIOR PRIOR FILING DATE: 2001-02-15
FRIOR PRIOR THING DATE: 2001-02-15
FRIOR PRIOR SEQ ID NOS: 9
SOFTWARE: FREESE 2001-02-15
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FREESE OF WINDOWS VERSION 4.0
SEQ ID NO 2
LENGTH: 2630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35.2%; Score 43; DB 7; Length 7968; 39.1%; Pred. No. 7.4e+02; tive 4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
35.2%; Score 43; DB 7; Length 2630;
Best Local Similarity 39.1%; Pred. No. 2.3e+02;
Matches 9; Conservative 4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7188 VAGYGTFAFGGDAGGMLGQGPMW 7210
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Best Local Similarity 39.17
Best Local 9; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
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            US-11-186-731-2
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RESULT 14
US-11-087-099-11993
Sequence 11993, Application US/11087099
Sequence 11993, Application US/11087099
September 11993, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53450) B EP

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Query Match
Best Local Similarity 56.2%; Pred. No. 45;
Matches 9; Conservative 2; Mismatches 2: Tradale 7
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Pred. No. 52;
1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: NACAHARI, KENJI
APPLICANT: MACAHARI, KENJI
APPLICANT: MACAHARI, KENJI
TITLE OF INVENTION: NOVAL Full length CDNA
FILLE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2001-11-05
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: March 7, 2006, 22:06:38 Job time : 10.4 secs
                                                                                                                                                                                                                          Sequence 2690, Application US/11072512
Publication No. US20060029945A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAMECHIKA, ICHIRO
SEKI, NAOHIKO
YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
                                                                                                                     179 GSGYTIALKTDGTLWT 194
                                                                                                                                                                                                                                                                                                                                                                                        ISHII, SHIZUKO
YAMAMOTO, JUN-ICHI
ISONO, YUUKO
HIO, YUKI
                                                                                                                                                                                                                                                                                      APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
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                                                                                            11 GSGFAIA---EGPLWT 23
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OTSUKA, KAORU
NAGAI, KEIICHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IRIE, RYOTARO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
, ORGANISM: Homo sapiens
US-11-072-512-2690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
```

protein search, using sw model OM protein March Run on:

7, 2006, 21:53:39; Search time 19.2 Seconds (without alignments) 120.271 Million cell updates/sec

US-10-751-235-10 122 1 LVAEVSEFLFGSGPAIAEGPLWTA 24

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

283416

DB seq length: 0 DB seq length: 200000000 Minimum I Maximum I

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database

PIR\_80:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

					SUMMARIES	
Result		Ouery				
No.	Score	Match	Match Length	DB	a	Description
1	118	96.7	995	7	T46159	cytochrome P450-li
7	26	45.9	324		B86819	oxidoreductase ypj
е	26	45.9	344		G84038	phenylalanyl-tRNA
4	52	45.1	350		AF2572	hypothetical prote
Ŋ		44.3	593		F86441	probable cytochrom
9	52	42.6	321		D97836	tetraacyldisacchar
7	20	41.0	350		AE1227 .	phenylajany-tRNA s
œ	20	41.0	350		AG1580	phenylalany-tRNA s
თ	49.5	40.6			G83838	oxidoreductase (sh
10	49	40.2			C83824	ABC transporter (p
11	49	0			D69472	nodulation protein
12	49	40.2			S75398	lysine-tRNA ligase
13	48	39.3	465	0	AC2843	multidrug efflux p
14.	48	39.3	465		D97620	hypothetical prote
15	48	39.3	493		P96696	protein FIN21.12
16	47	38.5	168		B85752	thiol peroxidase [
17	47	38.5	168		JC5504	
18	47	38.5	168		G90866	thiol peroxidase [
19	47	8	344		YFBSA	phenylalanine-tRNA
20	47	œ	354		AB2608	phenylalanyl-tRNA
21	47	38.5	360	0	A97390	phenylalanyl-tRNA
22	47	38.5	363		C87336	serine proteinase
23	47	∞ `	429		B83257	folylpolyglutamate
24	46	37.7	274		A25102	reaction center pr
25	46	37.7	337	7	AH0972	lipopolysaccharide
56	46	37.7	341	7	S33464	hypothetical prote
27	46	37.7	342	7	A96581	hypothetical prote
28	46	37.7	351	-	WWP2B	
59	46	37.7	351	-	WVPAS	coat protein VP2 -

succinate-semialde	protein CO5D11.1 [	translocon-associa	conserved hypothet	hypothetical prote	oxidoreductase hom	oxidoreductase hom	coat protein VP2 -	phenylalanine-tRNA	hypothetical prote	probable lipopolys	hypothetical prote	hydroxymethylgluta	probable glutamate	probable glutamate	hypothetical prote	
T31289	A88483	833294	AD2820	D97598	AE1158	AB1517	VVVP2J	AG3502	F86464	AB0470	G96554	S13887	T52043	T01200	T40527	
490 2	995 2	185 2	236 2	240 2	294 2	294 2	344 1	369 2	385 2	418 2	423 2	522 2	719 2	728 2	819 2	
37.7							36.9	36.9	36.9	36.9	36.9	36.9	36.9	36.9	36.9	
46	46	45	45	45	45	45	45	45	45	45	45	45	45	45	45	
30	31	32	33	34	32	36	37	38	33	40	41	42	43	44	45	

## ALIGNMENTS

		Aral	
		i	-
		protein	
		P450-like	
ULT 1	159	ochrome	

bidopsis thaliana

N'Alternate names: protein T4D2.60 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 09-Jul-2004

C,Accession: T46159
R;Nyakatura, G.; Fartmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.; N.; Asteria to the Protein Sequence Database, December 1999
A;Reference number: Z23025
A;Accession: T46159

A;Status: preliminary A;Molecule type: DNA A;Residues: 1-566 <NYA>

A;Cross-references: UNIPROT:09SCP8; UNIPARC:UPI00009D7F9; EMBL:AL132958
A;Experimental source: cultivar Columbia; BAC clone T4D2
C;Genetics:
A;Map position: 3
A;Introns: 183/2; 292/3; 358/3; 392/3; 439/3; 475/3; 503/2; 557/3
A;Note: T4D2.60
C;Superfamily: poa cytochrome P450 CYP97; cytochrome P450 homology
C;Keywords: heme; iron; metalloprotein
F;371-336/Domain: cytochrome P450 homology <P45>
F;514/Binding site: heme iron (Cys) (axial ligand) #status predicted

Gaps ö Query Match

96.7%; Score 118; DB 2; Length 566;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
Matches 23; Conservative 0; Mismatches 0; Indels

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144 LVAEVSEFLFGSGFAIAEGPLWT 166 1 LVAEVSEFLFGSGFAIAEGPLWT 23 ò g

RESULT 2

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oxidoreductase ypjF [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 09-Jul-2004
C;Accession: B86819
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlic
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp
A;Reference number: A86625; MUID:21235186; PMID:11337471 A;Cross=references: UNIPROT:Q9CFC7, UNIPARC:UP100000C6A7E, GB:AE005176, PID:g12724556, PI
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: ypjF A;Residues: 1-324 <STO> A,Accession: B86819 A,Status: preliminary A,Molecule type: DNA 0 E H B B A A A C 0 A 0

```
Chin, CW.; Chung, M.K.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, CW.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Mature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.L.; A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.L.; A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I. A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I. A;Authors: Saquence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
C,Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42.6%;
ilarity 52.4%;
Conservative
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Best Local Similarity
Matches 11; Conserv
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Best Local Similarity
Matches 8; Conserv
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A; Residues: 1-593 <STO>
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Hypothetical protein alr9005 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120ep
C; Species: Nostoc sp. PCC 7120
C; Species: Nostoc sp. etrain PCC 7120
A;Note: Nostoc sp. etrain PCC 7120
A;Note: Nostoc sp. etrain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AP5572
R;Kaneko, T: Namamra, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, B
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-350 «KUR>
A;Molecule type: DNA
A;Residues: 1-350 «KUR>
A;Cross-references: UNIPROT:Q8YJV8; UNIPARC:UPIO000CF069; GB:AP003605; PIDN:BAB77491.1;
A;Genetics:
A;Genetics:
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A;Genetics:
A;Genee: alr9005
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G84038
G94038
G94038
G96038
G96038
G9604
G; Species: Bacillus halodurans (strain C; Species: Dacilus halodurans (strain C; Species: Dac-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
G; Accession: G84038
G; Accession:
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45.9%; Score 56; DB 2; Length 344;
Best Local Similarity 47.4%; Pred. No. 0.49;
Matches 9; Conservative 4; Mismatches 6; Indels
                                                DB 2; Length 324;
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                                                                                                                                   5; Indels
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A;Gene: pheS
C;Superfamily: phenylalanine-tRNA ligase alpha chain
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                                                    Score 56; DB 2;
Pred. No. 0.46;
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Pred. No. 0.72;
0; Mismatches
                                                Query Match 45.9%; Score 56; DB Best Local Similarity 50.0%; Pred. No. 0.46 Matches 10; Conservative 5; Mismatches
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182 VLQFLFGTGFDAAKGIYWSS 201
                                                                                                                                                                                                                      5 VSEFLFGSGFAIAEGPLWTA 24
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114 ITEVEDLFIGLGFSVAEGP 132
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Best Local Similarity 61.1%;
Matches 11; Conservative
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А,Стовь-references: UNIPROT:Q9C6SO, UNIPARC:UPI00000AA2C9; GB:AE005172; NID:g11136728; РЛ
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C;Species: Rickettsia conorii
C;Species: Rickettsia conorii
C;Accession: D97836
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Rot Science 233, 2033-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:21442074; PMID:11557893
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A;Modecule type: DNA
A;Residues: 1-321 «KUR»
A;Cross-references: UNIPROT:Q92GN1; UNIPARC:UP1000012E92C; GB:AE006914; PIDN:AAL03630.1;
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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                             Gaps
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                                                                          A;Map position: 1
C;Superfamily: pea cytochrome P450 CYP97; cytochrome P450 homology
C;Keywords: heme; iron; metalloprotein
F;S14/Binding site: heme iron (Cys) (axial ligand) #status predicted
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Pred. No. 2;
4; Mismatches
                                                                                                                                                                                                                                      44.3%; Score 54; DB 2; ilarity 36.4%; Pred. No. 1.9; Conservative 7; Mismatches
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155 IVSVDSQRLFGNGFLIPAGPL 175
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RESULT 5 F86441 probable cytochrome P450 [imported] - Arabidopsis thaliana

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A;Gene: BH1511
C;Superfamily: short-chain dehydrogenase; short-chain alcohol dehydrogenase homology
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A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AE1227

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C;Species: Listeria innocus
C;Species: Listeria innocus
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AGISSO
C;Accession: AGISSO
Buchaud, B.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, Deminguez-Bernal; G.; Duchaud, B.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitcurnam, A.; Ma Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Reference number: ABI077; MUID:21537279; PMID:11679669
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R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Rese, 28, 4317-4317, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: G83838
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A;Experimental source: strain C-125
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C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 05-Oct-2004
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Pred. No. 4.5;
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C,Superfamily: phenylalanine-tRNA ligase alpha chain
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C;Superfamily: phenylalanine-tRNA ligase alpha chain
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Best Local Similarity 40.0%; Pred. No. 4.5;
Matches 8; Conservative 5; Mismatches
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A;Cross-references: UNIPROT:Q92CI7;
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nes 8; Conserva
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A,Molecule type: DNA
A,Residues: 1-287 <STO
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Best Local S
Matches · 8
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R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiran Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and the A;Reference number: A83650; WUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: D69472
R;Alenk, H.P.; (layton, R.A.; Tomb, J.F.; White, O.; Nelson, K.B.; Ketchum, K.A.; Dodson, R; Fleischmann, R.D.; Quackenbush, J.; Lee, NH.F.; Sutton, G.G.; Gill, S.; Kirkness, B.F., Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeor A;Reference number: A69250; MUID:98049343; PMID:9389475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:Q9KD24; UNIPARC:UPI00000D73F0; GB:AP001511; GB:BA000004; NID A;Experimental source: strain C-125
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A;Cross-references: UNIPROT:028493; UNIPARC:UP10000056BB8; GB:AE000979; GB:AE000782; NID
C;Superfamily: Rhizobium nodulation competitiveness protein nfeD
                                                                                                                                                                                                                                                                                                                                                      orter (permease) BH1395 [imported] - Bacillus halodurans (strain C-125) Bacillus halodurans
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C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                   C, Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
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                                                              Indels 3;
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   Length 287;
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40.2%; Score 49; DB 2; Length 287;
Best Local Similarity 40.0%; Pred. No. 5.2;
Matches 8; Conservative 5; Mismatches 7; Indels
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   DB 2;
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C,Superfamily: conserved hypothetical protein HI0360
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Pred. No. 8.4;
                               Pred. No. 4.3;
4; Mismatches
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   Score 49.5;
                                                                                                                                                                      202 LTRSLSESIVGQGIRVNGVAPGPIWT 227
                                                                                                                                1 LVAEVSEFLFGSGF---AIAEGPLWT 23
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124 DLMNYLFGSVIAVSRSDLWT 143
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Best Local Similarity 52.6%;
Matches 10; Conservative
Query Match
Best Local Similarity 38.5%;
Matches 10; Conservative
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A; Reference number: A97359; MUID:21608551; PMID:11743194
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Job time : 21.2 sec8
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A;Molecule type: DNA
A;Residues: 1-493 <STO>
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lysine-tRNA ligase (EC 6.1.1.6) - Sulfolobus solfataricus
NiAlternate names: lysyl-tRNA synthetase; protein c04032
C;Species: Sulfolobus solfataricus
C;Becies: Sulfolobus solfataricus
C;Becies: Sulfolobus solfataricus
C;Becies: 10-OC-1997 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004
C;Accession: S75398
R;Sensen, C.W.; Klenk, H.P.; Singh, R.K.; Allard, G.; Chan, C.C.Y.; Liu, Q.Y.; Penny, S. Moi. Microbiol: 22, 175-191, 1996
A;Title: Organizational characteristics and information content of an archaeal genome: 1 A;Reference number: S73076; MUD:97055432; PMID:8899719
A;Accession: S75398
A;Accession: S75398
A;Residues: 1-494 <SEN>
A;Residues: 1-494 <SEN>
A;Residues: 1-494 <SEN>
A;Residues: 1-494 <SEN>
A;Cross-references: UNIRROT:P99970; UNIPARC:UP10000136543; EMBL:Y08257; NID:g170772; PI
A;Experimental source: strain P2
A;Rocte: the nucleotide sequence was submitted to the EMBL Data Library, September 1996
C;Genetics:
B,Cross-references: Organizations and the EMBL Data Library, September 1996
B,Cross-references: Organizations and the EMBL Data Library, September 1996
B,Cross-references: Organizations and the EMBL Data Library, September 1996
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A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A;Acference number: AB2577; MUID:21608550; PMID:11743193

A;Accession: AC2643

A;Status: preliminary

A;Status: preliminary

A;Status: DNA

A;Residues: 1-465 «KUR>

A;Cross-references: UNIPROT:08UDF5; UNIPARC:UF10000DIDE3; GB:AE008688; PIDN:AAL43161.1;

A;Experimental source: strain C58 (Dupont)

C;Genetion:
A;Genee: Atu31.2

A;Map position: circular chromosome
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197620
hypothetical protein AGR C_3941 [imported] - Agrobacterium tumefaciens (strain C58, Cere C,Species: Agrobacterium tumefaciens
C,Species: Agrobacterium tumefaciens
C,Species: Agrobacterium tumefaciens
C,Facession: B97620
R,Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A,Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
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multidrug efflux protein (imported) - Agrobacterium tumefaciens (strain C58, Dupont)

C;Species Agrobacterium tumefaciens

C;Dacession: AC2843

C;Accession: AC2843

R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell, Science 294, 2317-2323, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
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C;Superfamily: lysine-tRNA ligase
C;Keywords: aminoacyl-tRNA synthetase; ATP; ligase; protein biosynthesis
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40.2%; Score 49; DB:
Best Local Similarity 38.1%; Pred. No. 9.5;
Matches 8; Conservative 5; Mismatches
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Pred. No.
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Best Local Similarity 57.1%;
Matches 8; Conservative
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71 FIFGSGFSVAVVPM 84
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A;Accession: D97620
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-465 <KUR>
A;Cross-references: UNIPROT:Q8UDFS; UNIPARC:UP10000D1DE3; GB:AE007869; PIDN:AAK87917.1;
A;Gene:ics:
A;Gene: AGR C 3941
A;Map position: circular chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ritheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C., A; Authors: Hunter, J.L.; Y.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwarz, C.M.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Rizzo, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Reference and analysis of chromosome 1 of the plant Arabidopsis.
A; Accession: F96696
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                 Score 48; DB
Pred. No. 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Map position: 1 .
C;Superfamily: glucose transport protein
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Best Local Similarity 57.1%;
Matches 8; Conservative
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71 FIFGSGFSVAVVPM 84
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